

# SEQUENCE LISTING

<110> Benjanin, Stephane  
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US4.DIV

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<141> 2001-11-13

<150> US 09/924,340

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<150> PCT/IB01/01715

<151> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

<151> 2001-06-15

<150> US 60/293,574

<151> 2001-05-25

<160> 112

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<222> 1965..1970

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<222> 2001..2016

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gccatcacca agaaccggaa catgcggaca ccctgatctc ggacttctag ccttcagaac 120  
cggttgccaca gttttgatga tcatctctct cccaaccaag atggtggaaa aagcaaaaac 180



20 25 30  
 Thr Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr  
 35 40 45  
 Met Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr  
 50 55 60  
 Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu  
 65 70 75 80  
 Glu Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu  
 85 90 95  
 Asp Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu  
 100 105 110  
 Ile Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met  
 115 120 125  
 Lys Gln Lys Gly Lys Lys  
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<210> 3  
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 <222> 1045..1050

<220>  
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 cgc tct ccc gtc ccg cgg tgg ttg ctg ctg ccg ctg ctg ctg ggc 104  
 Arg Ser Pro Val Pro Arg Trp Leu Leu Leu Pro Leu Leu Leu Gly  
 -15 -10 -5  
 ctg aac gca gga gct gtc att gac tgg ccc aca gag gag ggc aag gaa 152  
 Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu  
 1 5 10  
 gta tgg gat tat gtg acg gtc cgc aag gat gcc tac atg ttc tgg tgg 200  
 Val Trp Asp Tyr Val Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp  
 15 20 25  
 ctc tat tat gcc acc aac tcc tgc aag aac ttc tca gaa ctg ccc ctg 248  
 Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu  
 30 35 40 45  
 gtc atg tgg ctt cag ggc ggt cca ggc ggt tct agc act gga ttt gga 296  
 Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly  
 50 55 60  
 aac ttt gag gaa att ggg ccc ctt gac agt gat ctc aaa cca cgg aaa 344  
 Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys  
 65 70 75

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acc acc tgg ctc cag gct gcc agt ctc cta ttt gtg gat aat ccc gtg 392
Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val
80 85 90
ggc act ggg ttc agt tat gtg aat ggt agt ggt gcc tat gcc aag gac 440
Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp
95 100 105
ctg gct atg gtg gct tca gac atg atg gtt ctc ctg aag acc ttc ttc 488
Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
110 115 120 125
agt tgc cac aaa gaa ttc cag aca gtt cca ttc tac att ttc tca gag 536
Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu
130 135 140
tcc tat gga gga aaa atg gca gct ggc att ggt cta gag ctt tat aag 584
Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys
145 150 155
gcc att cag cga ggg acc atc aag tgc aac ttt gcg ggg gtt gcc ttg 632
Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu
160 165 170
ggg gat tcc tgg atc tcc cct gtt gat tgc gtg ctc tcc tgg gga cct 680
Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro
175 180 185
tac ctg tac agc atg tct ctt ctc gaa gac aaa ggt ctg gca gag gtg 728
Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val
190 195 200 205
tct aag gtt gca gag caa gta ctg aat gcc gta aat aag ggg ctc tac 776
Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr
210 215 220
aga gag gcc aca gag ctg tgg ggg aaa gca gaa atg atc att gaa cag 824
Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln
225 230 235
gta aaa agg gga aac act cag agg cta gcc tgc ttg gct ttt tct ggt 872
Val Lys Arg Gly Asn Thr Gln Arg Leu Ala Cys Leu Ala Phe Ser Gly
240 245 250
ggg tac agg gcc cat ggt tgg tgt tgt caa act tgg agt cta cac 917
Gly Tyr Arg Ala His Gly Trp Cys Cys Gln Thr Trp Ser Leu His
255 260 265
tgaggctccc cacatatctg caaatgattg catgctggat aataaatctc ttgggtctaa 977
gcagtgatgt agtggctcct tacagagtca gaaagccacc caggcctgca agacttgctt 1037
gtccttcact aaatgtatgg attctattaa aaaaaaaaaa aaaa 1081

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<210> 4
<211> 293
<212> PRT
<213> Homo sapiens

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<221> SIGNAL
<222> 1..26

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-25 -20 -15
Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp Trp Pro
-10 -5 1 5
Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
10 15 20
Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn
25 30 35
Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly
40 45 50
Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser
55 60 65 70
Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu

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<221> 3'UTR  
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<221> polyA_signal  
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<222> 423..438
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<400> 5
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tgagtaaaag gactcagcca act atg aag ttt ttt gtc ttt gct tta gtc ttg 113
                Met Lys Phe Phe Val Phe Ala Leu Val Leu
                        -15                               -10
gct ctc atg att tcc atg att agc gct gat tca cat gaa aag aga cat 161
Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His
                        -5                               1                               5
cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209
His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile
                        10                               15                               20
aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257

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Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu
25          30          35          40
aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305
Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
          45          50          55
tca att gtc act tgatgatata attgcaattt aaactggttaa gctgtgttca 357
Ser Ile Val Thr
          60
gtactgtttc tgaataatag aaatcacttc tctaaaagca ataaatttca agcacatttt 417
taaataaaaa aaaaaaaaaa a 438

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<210> 6
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<213> Homo sapiens

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<222> 1..19

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<400> 6
Met Lys Phe Phe Val Phe Ala Leu Val Leu Ala Leu Met Ile Ser Met
          -15          -10          -5
Ile Ser Ala Asp Ser His Glu Lys Arg His His Gly Tyr Arg Arg Lys
          1          5          10
Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
          15          20          25
Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu
30          35          40          45
Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe Ser Ile Val Thr
          50          55

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<210> 7
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<212> DNA
<213> Homo sapiens

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<220>
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<220>
<221> polyA_signal
<222> 928..933

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<220>
<221> polyA_site
<222> 953..968

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          Met Arg Leu Pro Ala Gln Leu
          -15
ctg ggg ctg cta atg ctc tgg gtc tct gga tcc agt ggg gat att gtg 100
Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val

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ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529  
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu  
 65 70 75  
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574  
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser  
 80 85 90  
 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634  
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694  
 aagtgtcttt tccaaggcca agctcctgag ggcagg 730

<210> 10  
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 <212> PRT  
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<220>  
 <221> SIGNAL  
 <222> 1..14

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 -10 -5 1  
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile  
 5 10 15  
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser  
 20 25 30  
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg  
 35 40 45 50  
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp  
 55 60 65  
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser  
 70 75 80  
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser  
 85 90

<210> 11  
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<220>  
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<220>  
 <221> CDS  
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<220>  
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 tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgt 120  
 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180  
 gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccctt 240  
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289  
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala  
 -10 -5  
 aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337  
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly  
 1 5 10 15

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atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
                20                25                30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
                35                40                45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
                50                55                60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
                65                70                75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
80                85                90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcaggtg 694
aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

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<210> 12
<211> 107
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..14

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<400> 12
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                -10                -5                1
Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
                5                10                15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
                20                25                30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35                40                45                50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
                55                60                65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
                70                75                80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
                85                90

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<210> 13
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<212> DNA
<213> Homo sapiens

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<220>
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<222> 254..574

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<220>
<221> 3'UTR
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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180  
 gccctcaggc ctccaggcctt ccctggcttg aagattgggc ttcacctggg acctaccctt 240  
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289

Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala

-10

-5

aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337  
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly  
 1 5 10 15

atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385  
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys  
 20 25 30

ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433  
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys  
 35 40 45

tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481  
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser  
 50 55 60

ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529  
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu  
 65 70 75

agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574  
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser  
 80 85 90

tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634  
 ctttgaaatg taggtagctt attatccaca ttttgcagat gaggaacag agtcaggtga 694  
 agtgtctttt ccaaggccaa gctcctgagg gcaggggc 732

<210> 14

<211> 107

<212> PRT

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<220>

<221> SIGNAL

<222> 1..14

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-10

-5

1

Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile

5

10

15

Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser

20

25

30

Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg

35

40

45

50

Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp

55

60

65

Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser

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75

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Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser

85

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<210> 15

<211> 733

<212> DNA

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<221> CDS  
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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180  
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccct 240  
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289  
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala  
 -10 -5  
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337  
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly  
 1 5 10 15  
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385  
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys  
 20 25 30  
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433  
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys  
 35 40 45  
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481  
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser  
 50 55 60  
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529  
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu  
 65 70 75  
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574  
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser  
 80 85 90  
 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634  
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694  
 aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

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<220>  
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 <222> 1..14

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 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile  
 5 10 15  
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser  
 20 25 30  
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg  
 35 40 45 50  
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp  
 55 60 65  
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser  
 70 75 80  
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser  
 85 90

<210> 17

<211> 1175  
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<220>  
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 <222> 1014..1175

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 <222> 1131..1136

<220>  
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 <222> 1160..1175

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 aacccttcg agcaagacgt ggtgatgcc aattggtggaa aggagaaaat cacagaggaa 180  
 taggactttt cccatccaat tttgtaacaa ctaatttaaa catagagact gaggcagcgg 240  
 ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg 300  
 agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag 353  
 Met Asp Arg Ala Leu Gln Val Leu Gln  
 1 5  
 agt ata gat cca aca gat tca aaa cca gac tcc caa gac ctt ttg gat 401  
 Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp  
 10 15 20 25  
 tta gaa gat atc tgc caa cag atg ggt cca atg ata gat gaa aaa ctt 449  
 Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu  
 30 35 40  
 gaa gaa att gat agg aag cat tca gaa ttg tct gaa ttg aat gtt aaa 497  
 Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys  
 45 50 55  
 gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca 545  
 Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro  
 60 65 70  
 gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct 593  
 Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro  
 75 80 85  
 gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt 641  
 Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly  
 90 95 100 105  
 gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689  
 Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser  
 110 115 120  
 tat agc cta gga ccc gat caa att ggt cca ctg aga tct ctg cct cca 737  
 Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro  
 125 130 135  
 aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785  
 Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu  
 140 145 150  
 agc act gga caa gac act gtt tcc aat cct act tat atg aac cag aac 833  
 Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn  
 155 160 165

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tct aac cta cag tca gct act ggt aca act gct tac aca cag caa atg      881
Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met
170                               175          180          185
ggg atg tct gtg gat atg tca tct tat cag aac act act tcc aat ttg      929
Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu
                               190          195          200
cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca      977
Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
                               205          210          215
cag cag cac aca aat tac cat cag cag cct ctc ctt tagaaacaaa      1023
Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
                               220          225
tcaagcattt tcttgaaagc cttcataagt gtattattca gtccttgtga taccaacctg 1083
aaaatattaa aacttttttc cctctcaact caaaggacc atgaataaat aaagcacaaa 1143
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<211> 229

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<213> Homo sapiens

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Lys Pro Asp Ser Gln Asp Leu Leu Asp Leu Glu Asp Ile Cys Gln Gln
                               20          25          30
Met Gly Pro Met Ile Asp Glu Lys Leu Glu Glu Ile Asp Arg Lys His
                               35          40          45
Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
                               50          55          60
Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
65                               70          75          80
Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
                               85          90          95
Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser
                               100          105          110
Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
                               115          120          125
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
130                               135          140
Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
145                               150          155          160
Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
                               165          170          175
Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
                               180          185          190
Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
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Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
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Gln Gln Pro Leu Leu
225

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 Met Arg  
 -15  
 gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc 165  
 Ala Trp Ile Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala  
 -10 -5 1  
 cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213  
 Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr  
 5 10 15  
 gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg 261  
 Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val  
 20 25 30  
 gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg 309  
 Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val  
 35 40 45 50  
 gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg 357  
 Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val  
 55 60 65  
 tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405  
 Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro  
 70 75 80  
 acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453  
 Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn  
 85 90 95  
 gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501  
 Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys  
 100 105 110  
 acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549  
 Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile  
 115 120 125 130  
 ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa 597  
 Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu  
 135 140 145  
 ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645  
 Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu  
 150 155 160  
 tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg 693  
 Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu  
 165 170 175  
 cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac 741  
 Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp  
 180 185 190  
 cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg 789  
 His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg  
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 Lys Ala Lys Ile Lys Ser Glu Met  
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 Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val  
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 Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu  
                           35                          40                          45  
 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly  
                           50                          55                          60  
 Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln  
   65                          70                          75  
 Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys  
  80                          85                          90                          95  
 Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr  
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 Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp  
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 Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu  
                           130                          135                          140  
 Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val  
  145                          150                          155  
 Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln  
  160                          165                          170                          175  
 Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala  
                           180                          185                          190  
 Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser  
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<220>  
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 gctaaa atg aag act ctg cag tct aca ctt ctc ctg tta ctg ctt gtg 168  
           Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val  
                           -15                          -10                          -5  
 cct ctg ata aag cca gca cca cca acc cag cag gac tca cgc att atc 216  
 Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile  
                           1                          5                          10



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Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp	
15 20 25	
tat gag gat aaa tac ctg gat gga aaa aat att aag gaa aaa gaa act	312
Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr	
30 35 40	
gtg ata ata ccc aat gag aaa agt ctt caa tta caa aaa gat gag gca	360
Val Ile Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala	
45 50 55 60	
ata aca cca tta cct ccc aag aaa gaa aat gat gaa atg ccc acg tgt	408
Ile Thr Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys	
65 70 75	
ctg ctg tgt gtt tgt tta agt ggc tct gta tac tgt gaa gaa gtt gac	456
Leu Leu Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp	
80 85 90	
att gat gct gta cca ccc tta cca aag gaa tca gcc tat ctt tac gca	504
Ile Asp Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala	
95 100 105	
cga ttc aac aaa att aaa aag ctg act gcc aaa gat ttt gca gac ata	552
Arg Phe Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile	
110 115 120	
cct aac tta aga aga ctc gat ttt aca gga aat ttg ata gaa gat ata	600
Pro Asn Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile	
125 130 135 140	
gaa gat ggt act ttt tca aaa ctt tct ctg tta gaa gaa ctt tca ctt	648
Glu Asp Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu	
145 150 155	
gct gaa aat caa cta cta aaa ctt cca gtt ctt cct ccc aag ctc act	696
Ala Glu Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr	
160 165 170	
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Leu Phe Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala	
175 180 185	
aat gca ttc aaa aaa ctg aat aac ctc acc ttc ctc tac ttg gac cat	792
Asn Ala Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His	
190 195 200	
aat gcc ctg gaa tcc gtg cct ctt aat tta cca gaa agt cta cgt gta	840
Asn Ala Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val	
205 210 215 220	
att cat ctt cag ttc aac aac ata gct tca att aca gat gac aca ttc	888
Ile His Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe	
225 230 235	
tgc aag gct aat gac acc agt tac atc cgg gac cgc att gaa gag ata	936
Cys Lys Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile	
240 245 250	
cgc ctg gag ggc aat cca atc gtc ctg gga aag cat cca aac agt ttt	984
Arg Leu Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe	
255 260 265	
att tgc tta aaa aga tta ccg ata ggg tca tac ttt taacctctat	1030
Ile Cys Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe	
270 275 280	
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ggaacttaag tattgggtta atattaacct tgatatcat tttgaaggaa tttaatat	1150
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actaccat	1330
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aactttg	1570
atagcagata gtctcatatt taggaaaact ttccaaataa aataaatgtt attctctgat	1630
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at	1750

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tctatggcaa agtcttttcaa atacgagata actgcaaaat attttccttt tatactacag 1870  
aaatgagaat ctcacataa aattagttca agcataagat gaaaacagaa tattctgtgg 1930  
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Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile  
30 35 40 45  
Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr  
50 55 60  
Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu  
65 70 75  
Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp  
80 85 90  
Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe  
95 100 105  
Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile Pro Asn  
110 115 120 125  
Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile Glu Asp  
130 135 140  
Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu  
145 150 155  
Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe  
160 165 170  
Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala  
175 180 185  
Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala  
190 195 200 205  
Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His  
210 215 220  
Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys  
225 230 235  
Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu  
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Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe  
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 Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val  
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 ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147  
 Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val  
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 agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc 195  
 Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala  
                   35                  40                  45  
 atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc 243  
 Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly  
           50                  55                  60  
 atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg 291  
 Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro  
           65                  70                  75  
 gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc 339  
 Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu  
           80                  85                  90  
 ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa 387  
 Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu  
           95                  100                  105                  110  
 gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac 435  
 Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His  
                   115                  120                  125  
 tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg 483  
 Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp  
           130                  135                  140  
 tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg 531  
 Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu  
           145                  150                  155  
 aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579  
 Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser  
           160                  165                  170  
 ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc 627  
 Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val  
           175                  180                  185                  190  
 aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc 675  
 Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe  
                   195                  200                  205  
 tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg 723  
 Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp  
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225 230 235
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg 819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
240 245 250
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca 867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
255 260 265 270
cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc 915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
275 280 285
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc 963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
290 295 300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc cct 1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
305 310 315
ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca cag aca 1059
Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
320 325 330
gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc 1107
Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
335 340 345 350
gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg cgc tgc 1155
Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
355 360 365
ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc 1203
Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser
370 375 380
ctg ctg aag tgaggaggcc catgggcaga agatagggat tcccctggac 1252
Leu Leu Lys
385
cacacctcgc tgggttactt tggtcacaag taggagacac agatggcacc tgtggccaga 1312
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aaaaaaaaaaaa 1746

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 <213> Homo sapiens

<220>  
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 Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile  
 20 25 30  
 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr  
 35 40 45  
 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu  
 50 55 60

Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro  
 65 70 75  
 Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser  
 80 85 90 95  
 Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu  
 100 105 110  
 Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu  
 115 120 125  
 Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr  
 130 135 140  
 Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met  
 145 150 155  
 Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr  
 160 165 170 175  
 Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser  
 180 185 190  
 Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu  
 195 200 205  
 Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile  
 210 215 220  
 Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser  
 225 230 235  
 Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp  
 240 245 250 255  
 Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser  
 260 265 270  
 Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val  
 275 280 285  
 Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys  
 290 295 300  
 His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val  
 305 310 315  
 Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu  
 320 325 330 335  
 Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu  
 340 345 350  
 Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg  
 355 360 365  
 Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu  
 370 375 380  
 Lys

<210> 25  
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 <212> DNA  
 <213> Homo sapiens

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 <222> 1..126

<220>  
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 <222> 127..879

<220>  
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 <222> 880..1239

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 <222> 1224..1239

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ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
            -20            -15            -10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
            -5            1            5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca 264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
            10            15            20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat 312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
            25            30            35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag 360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
40            45            50            55
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc 408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
            60            65            70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg 456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
            75            80            85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc 504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
            90            95            100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag 552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
            105            110            115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg 600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Tyr Ser Gln Phe Leu
120            125            130            135
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca 648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
            140            145            150
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg 696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
            155            160            165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc cgg gcc tcc tgt 744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
            170            175            180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac 792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
            185            190            195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga 840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
200            205            210            215
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggtcgct 889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
            220            225
ggaagggcac cctctttaac ccatccctca gcaaacgcag ctcttcccaa ggaccaggtc 949
ccttgacgtt ccgaggatgg gaaagggtgac aggggcatgt atggaatttg ctgcttctct 1009
gggggtccctt ccacaggagg tcctgtgaga accaaccttt gaggcccaag tcatgggggtt 1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa 1129
ctagaaaattt ccccttcattg aaggtagaga gaaggggtct ctcccaacat atttctcttc 1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa 1239

<210> 26
<211> 251
<212> PRT
<213> Homo sapiens

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<220>

<221> SIGNAL

<222> 1..24

<400> 26

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-5 1 5  
Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg  
10 15 20  
Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala  
25 30 35 40  
Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala  
45 50 55  
Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met  
60 65 70  
Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn  
75 80 85  
Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His  
90 95 100  
Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala  
105 110 115 120  
Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg  
125 130 135  
Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg  
140 145 150  
His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val  
155 160 165  
Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln  
170 175 180  
Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu  
185 190 195 200  
Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly  
205 210 215  
Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile  
220 225

<210> 27

<211> 1179

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..115

<220>

<221> CDS

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<220>

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<222> 1145..1150

<220>

<221> polyA\_site

<222> 1164..1179

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tgggtctctg actcacttct gacttttaggc gctcgaggac tgtgcccagg agcag atg 118
Met
1
cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa 166
Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln
5 10 15
cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt 214
Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu
20 25 30
gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag 262
Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln
35 40 45
tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga 310
Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly
50 55 60 65
ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat 358
Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr
70 75 80
tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct 406
Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser
85 90 95
gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc 454
Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly
100 105 110
ttt gga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa 502
Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys
115 120 125
aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac 550
Asn Leu His Phe Leu Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp
130 135 140 145
ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc 598
Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe
150 155 160
aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat 646
Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr
165 170 175
tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg 694
Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val
180 185 190
cag tgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga 742
Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg
195 200 205
gat cat gac aac tat gaa ggg aac tgc gca gaa gat cag tct ggc 790
Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly
210 215 220 225
tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac 838
Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr
230 235 240
agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc 886
Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr
245 250 255
tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg 934
Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg
260 265 270
cca aat gat ttt att cca aat gta att taattgctgc tggtgggctt 981
Pro Asn Asp Phe Ile Pro Asn Val Ile
275 280
tcgtttctgc aattcagctt tgtttaaagt gatttgaaaa atactcattc tgaacatatac 1041
catgcgcaat catgataact gttgtgagta gtgcttttca ttcttctcac ttgcctttgt 1101
tacttaatgt gctttcagta cagcagatat gcaatattca ccaaataaat gtagactgtg 1161
tcaaaaaaaaa aaaaaaaaaa 1179

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<210> 28  
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 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> 116  
 <223> Xaa = Asn,Thr

<220>  
 <221> UNSURE  
 <222> 233  
 <223> Xaa = Phe,Ser

<400> 28  
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 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe  
 20 25 30  
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg  
 35 40 45  
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser  
 50 55 60  
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val  
 65 70 75 80  
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg  
 85 90 95  
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn  
 100 105 110  
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn  
 115 120 125  
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile  
 130 135 140  
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn  
 145 150 155 160  
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu  
 165 170 175  
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu  
 180 185 190  
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp  
 195 200 205  
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser  
 210 215 220  
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr  
 225 230 235 240  
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr  
 245 250 255  
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile  
 260 265 270  
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile  
 275 280

<210> 29  
 <211> 1118  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..344

<220>  
 <221> CDS  
 <222> 345..1118

<220>  
 <221> polyA\_site  
 <222> 1103..1118

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 tgggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180  
 aacccttggg gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240  
 cggccgcag tagctgcaga ctccgccgc gacgtgtgcg cgcttctctg ggccagagcg 300  
 agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356  
 Met Gly Arg Thr  
 cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404  
 Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala  
 -15 -10 -5 1  
 tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452  
 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys  
 5 10 15  
 atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500  
 Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val  
 20 25 30  
 gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548  
 Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala  
 35 40 45  
 aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596  
 Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu  
 50 55 60 65  
 gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644  
 Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser  
 70 75 80  
 gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692  
 Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys  
 85 90 95  
 gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740  
 Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile  
 100 105 110  
 tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788  
 Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg  
 115 120 125  
 ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836  
 Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg  
 130 135 140 145  
 gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884  
 Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala  
 150 155 160  
 cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932  
 Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr  
 165 170 175  
 aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980  
 Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn  
 180 185 190  
 atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028  
 Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val  
 195 200 205  
 act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076  
 Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg  
 210 215 220 225  
 gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa aaa 1118  
 Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys

<210> 30  
 <211> 258  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..20

<220>  
 <221> UNSURE  
 <222> 49  
 <223> Xaa = Glu, \*

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 1 5 10  
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser  
 15 20 25  
 Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala  
 30 35 40  
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val  
 45 50 55 60  
 Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser  
 65 70 75  
 Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe  
 80 85 90  
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg  
 95 100 105  
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys  
 110 115 120  
 Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg  
 125 130 135 140  
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys  
 145 150 155  
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe  
 160 165 170  
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln  
 175 180 185  
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu  
 190 195 200  
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln  
 205 210 215 220  
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys  
 225 230 235  
 Lys Lys

<210> 31  
 <211> 1273  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..13

<220>  
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 <222> 14..1048

<220>  
 <221> 3'UTR  
 <222> 1049..1273

<220>  
 <221> polyA\_signal  
 <222> 1234..1239

<220>  
 <221> polyA\_site  
 <222> 1258..1273

<400> 31  
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                   -25                  -20                  -15  
 tgc ggc cag gcg tgg ggt gcg tcg gtg ggc ggc cgc agc tgc gag gag 97  
 Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu  
                   -10                  -5                  1  
 ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac 145  
 Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn  
                   5                  10                  15  
 ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt 193  
 Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val  
                   20                  25                  30                  35  
 gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga 241  
 Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg  
                   40                  45                  50  
 agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc 289  
 Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro  
                   55                  60                  65  
 tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt 337  
 Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe  
                   70                  75                  80  
 aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg 385  
 Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu  
                   85                  90                  95  
 aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg 433  
 Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu  
                   100                  105                  110                  115  
 gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac 481  
 Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn  
                   120                  125                  130  
 aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att 529  
 Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile  
                   135                  140                  145  
 ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg 577  
 Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu  
                   150                  155                  160  
 cag cgg aca atg atc aga tat ttc aca tcg aat cca gcc tca aag gtc 625  
 Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val  
                   165                  170                  175  
 ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt 673  
 Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe  
                   180                  185                  190                  195  
 cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata 721  
 His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile  
                   200                  205                  210  
 gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca 769  
 Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala  
                   215                  220                  225  
 ggt gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga 817

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ala Met Asp Thr Ala Gly  
                                  250                      255                      260  
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly  
                                  265                      270                      275  
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp  
                                  280                      285                      290  
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn  
 295                      300                      305                      310  
 Gly Pro Lys Lys Gly Gly Ser Lys  
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                                  Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val  
                                  1                      5                      10  
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159  
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser  
                                  15                      20                      25  
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207  
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg  
                                  30                      35                      40                      45  
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255  
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr  
                                  50                      55                      60  
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303  
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro  
                                  65                      70                      75  
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351  
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val  
                                  80                      85                      90  
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399  
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr  
                                  95                      100                      105  
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447

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Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
110          115          120          125
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
          130          135          140
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
          145          150          155
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
          160          165          170
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
          175          180          185
cac tca gag gat tgt gat gaa caa tgt tgt tgactagcac tgtgagaata 692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
190          195          200
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          20          25          30
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
          35          40          45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
          50          55          60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
          65          70          75          80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
          85          90          95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
          100          105          110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
          115          120          125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
          130          135          140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
          145          150          155          160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
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Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
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Asp Cys Asp Cys Glu Gln Cys Cys
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taaattctgc caaaaggact gaggaacggt gcctggaaaaa gggcaagaat atcacggc 118
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaaa ctatccagtg 695
Gly Pro Tyr
atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggg 755
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 Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Asn Ala  
 35 40 45  
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 gcctcacttc gtccactgt ggtaggggt ggtcctgcg aatgttaagt gatttgctca 180  
 aggtgcccat ttgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240  
 aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292  
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu  
 -15 -10  
 ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340  
 Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp  
 -5 1 5  
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388  
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met  
 10 15 20  
 ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436  
 Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr  
 25 30 35 40  
 gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tcg tgg gtg ggg ccc 484  
 Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro

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aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532
Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe
      60      70
gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580
Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His
      75      80      85
gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc 628
Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr
      90      95      100
act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc 676
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe
      105      110      115      120
ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc 724
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile
      125      130      135
cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc 772
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val
      140      145      150
att tcg ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc 820
Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr
      155      160      165
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc 868
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr
      170      175      180
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg 916
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu
      185      190      195      200
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag 964
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln
      205      210      215
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac 1012
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr
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gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgctc 1058
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp
      235      240
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ggacttcctc tacttctcct tgctggatca gggccttcct gcctcccgtc gggcaggtct 1178
ggccttgctc tcttggcagg gccccagccc ctctgaccac tctgcagctc accatgcagc 1238
tgatgccaaa gttgtggtgt ccagtgtgca gcagccctgg gagccactgc caccttcaga 1298
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tctccaaaga cgcactgcca ggtcccaagc ttcagactgc tgtgcttagt aagcaagtga 1538
gaagcctggg gtttgagacc cacctactct ctggcagcat cagcatccta ctctggcaa 1598
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 Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro  
           15                  20                  25  
 Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu  
       30                  35                  40  
 Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys  
 45                  50                  55                  60  
 Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val  
                   65                  70                  75  
 Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn  
           80                  85                  90  
 Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe  
       95                  100                  105  
 Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala  
      110                  115                  120  
 Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly  
 125                  130                  135                  140  
 Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn  
                   145                  150                  155  
 Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser  
           160                  165                  170  
 Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val  
      175                  180                  185  
 Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys  
      190                  195                  200  
 Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu  
 205                  210                  215                  220  
 Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly  
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 Arg Gln Pro Tyr Lys Ser Trp  
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                   Met Pro Ala Cys Arg Leu Gly Pro

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cta gcc gcc gcc ctc ctc ctc agc ctg ctg ctg ttc ggc ttc acc cta 162
Leu Ala Ala Ala Leu Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu
-20 -15 -10
gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210
Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln
-5 1 5 10
gct gac cag aac tgc acg caa gag tgc gtc tcg gac agc gaa tgc gcc 258
Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
15 20 25
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
30 35 40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
45 50 55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
60 65 70 75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
80 85 90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
95
agttttctgcc tggccctgca tctgggtcca gccacactgc cctcccccttt ttcgggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaa aaaaaaaaaa a 643

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<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..30

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-30 -25 -20 -15
Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
-10 -5 1
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
5 10 15
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
20 25 30
Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
35 40 45 50
Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
55 60 65
Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
70 75 80
Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
85 90

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<210> 43
<211> 501
<212> DNA
<213> Homo sapiens

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<220>
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<220>  
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 agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120  
 ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180  
 ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236  
 Met Gln Gly  
 -30  
 act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284  
 Thr Pro Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg  
 -25 -20 -15  
 aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332  
 Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met  
 -10 -5 1  
 aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380  
 Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys  
 5 10 15  
 cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428  
 Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val  
 20 25 30 35  
 gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476  
 Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg  
 40 45 50  
 gtt cct ttc tcc gaa ctg aaa gac a 501  
 Val Pro Phe Ser Glu Leu Lys Asp  
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 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 1..33

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 Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu  
 -15 -10 -5  
 Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys  
 1 5 10 15  
 Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro  
 20 25 30  
 Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val  
 35 40 45  
 Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp  
 50 55

<210> 45  
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 <212> DNA  
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<220>  
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 Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys  
 35 40 45  
 Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser  
 50 55 60  
 Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu  
 65 70 75 80  
 Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu  
 85 90 95  
 Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys  
 100 105 110  
 Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp  
 115 120 125  
 Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala  
 130 135 140  
 Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys  
 145 150 155 160  
 Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro  
 165 170 175  
 Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly  
 180 185 190  
 Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln  
 195 200 205  
 Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser  
 210 215 220  
 Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp  
 225 230 235 240  
 Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys  
 245 250 255  
 Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly  
 260 265 270  
 Trp Gly Trp Gly Gln Gly Phe  
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 ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180  
 ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240  
 gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293  
 Met Ile Tyr Thr Met Lys Lys Val His  
 -25 -20  
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 -15 -10 -5  
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 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp  
 1 5 10  
 acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437  
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys  
 15 20 25 30  
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 Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn  
 35 40 45  
 att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533  
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly  
 50 55 60  
 aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581  
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr  
 65 70 75  
 aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629  
 Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys  
 80 85 90  
 cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677  
 Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys  
 95 100 105 110  
 gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725  
 Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu  
 115 120 125  
 aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773  
 Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe  
 130 135 140  
 cag gtg gat aat tat gga acc cag ctg aat gct gtg aat aac tcc ctg 821  
 Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu  
 145 150 155  
 act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869  
 Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro  
 160 165 170  
 tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917  
 Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu  
 175 180 185 190  
 aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965  
 Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys  
 195 200 205  
 tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013  
 Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu  
 210 215 220  
 tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061

Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly  
           225                          230                          235  
 ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109  
 Gly Leu Ile Lys Thr Lys Arg Lys Lys Arg Lys Gln Arg Val Lys Ile  
           240                          245                          250  
 gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt 1159  
 Ala Tyr Glu Glu Ile Phe Val Lys Asn Met  
           255                          260  
 aacattaatt ctactaaata ttttatatga aatgtttcac tatgattttc tatttttctt 1219  
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 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys  
   5                          10                          15                          20  
 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys  
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 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu  
                           40                          45                          50  
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser  
                           55                          60                          65  
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys  
                           70                          75                          80  
 Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr  
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 Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly  
                           105                          110                          115  
 Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn  
                           120                          125                          130  
 Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr  
                           135                          140                          145  
 Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val  
                           150                          155                          160  
 Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala  
   165                          170                          175                          180  
 Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser  
                           185                          190                          195  
 Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn  
                           200                          205                          210  
 Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys  
                           215                          220                          225  
 Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg  
                           230                          235                          240  
 Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val  
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 Lys Asn Met

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<222> 1179..1194

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Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20                               -15          -10          -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag      152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
                               1              5              10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa      200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
                               15              20              25
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc      248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
                               30              35              40
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta      296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
                               45              50              55              60
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc      344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
                               65              70              75
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac      392
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
                               80              85              90
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag      440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
                               95              100             105
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt      488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
                               110             115             120
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag      536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
                               125             130             135             140
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag      584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
                               145             150             155
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg      632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
                               160             165             170
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg      680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
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175	180	185	
cct gat gag ggg aaa cta	cag cac ctg gaa aat	gaa ctc acc cac gat	728
Pro Asp Glu Gly Lys Leu	Gln His Leu Glu Asn	Glu Leu Thr His Asp	
190	195	200	
atc atc acc aag ttc ctg	gaa aat gaa gac aga	agg tct gcc agc tta	776
Ile Ile Thr Lys Phe Leu	Glu Asn Glu Asp Arg	Arg Ser Ala Ser Leu	
205	210	215	220
cat tta ccc aaa ctg tcc	att act gga acc tat	gat ctg aag agc gtc	824
His Leu Pro Lys Leu Ser	Ile Thr Gly Thr Tyr	Asp Leu Lys Ser Val	
225	230	235	
ctg ggt caa ctg ggc atc	act aag gtc ttc agc	aat ggg gct gac ctc	872
Leu Gly Gln Leu Gly Ile	Thr Lys Val Phe Ser	Asn Gly Ala Asp Leu	
240	245	250	
tcc ggg gtc aca gag gag	gca ccc ctg aag ctc	tcc aag gcc gtg cat	920
Ser Gly Val Thr Glu Glu	Ala Pro Leu Lys Leu	Ser Lys Ala Val His	
255	260	265	
aag gct gtg ctg acc atc	gac gag aaa ggg act	gaa gct gct ggg gcc	968
Lys Ala Val Leu Thr Ile	Asp Glu Lys Gly Thr	Glu Ala Ala Gly Ala	
270	275	280	
atg ttt tta gag gcc ata	ccc atg tct atc ccc	ccc gag gtc aag ttc	1016
Met Phe Leu Glu Ala Ile	Pro Met Ser Ile Pro	Pro Glu Val Lys Phe	
285	290	295	300
aac aaa ccc ttt gtc ttc	tta atg att gac caa	aat acc aag tct ccc	1064
Asn Lys Pro Phe Val Phe	Leu Met Ile Asp Gln	Asn Thr Lys Ser Pro	
305	310	315	
ctc ttc atg gga aaa gtg	gtg aat ccc acc caa	aaa taactgcctc	1110
Leu Phe Met Gly Lys Val	Val Asn Pro Thr Gln	Lys	
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				-5				1				5			
Ile	Leu	Glu	Gly	Leu	Asn	Phe	Asn	Leu	Thr	Glu	Ile	Pro	Glu	Ala	Gln
	10				15					20					
Ile	His	Glu	Gly	Phe	Gln	Glu	Leu	Leu	Arg	Thr	Leu	Asn	Gln	Pro	Asp
25					30					35				40	
Ser	Gln	Leu	Gln	Leu	Thr	Thr	Gly	Asn	Gly	Leu	Phe	Leu	Ser	Glu	Gly
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Leu	Lys	Leu	Val	Asp	Lys	Phe	Leu	Glu	Asp	Val	Lys	Lys	Leu	Tyr	His
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Ser	Glu	Ala	Phe	Thr	Val	Asn	Phe	Gly	Asp	Thr	Glu	Glu	Ala	Lys	Lys
		75				80						85			
Gln	Ile	Asn	Asp	Tyr	Val	Glu	Lys	Gly	Thr	Gln	Gly	Lys	Ile	Val	Asp
	90				95					100					
Leu	Val	Lys	Glu	Leu	Asp	Arg	Asp	Thr	Val	Phe	Ala	Leu	Val	Asn	Tyr
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Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val	Lys	Asp	Thr
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Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Val	Thr	Thr	Val	Lys	Val	Pro
			140					145					150		



His	Thr	Ile	Ile	Thr	Asp	Thr	Glu	Leu	Pro	Pro	Leu	Lys	Leu	Met	His	
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Ser	Phe	Cys	Ala	Phe	Lys	Ser	Asp	Asp	Gly	Pro	Cys	Lys	Ala	Ile	Met	
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aaa	aga	ttt	ttc	ttc	aat	att	ttc	act	cga	cag	tgc	gaa	gaa	ttt	ata	538
Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg	Gln	Cys	Glu	Glu	Phe	Ile	
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tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	ttt	gaa	agt	ctg	gaa	gag	58
Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser	Leu	Glu	Glu	
			60					65					70			
tgc	aaa	aaa	atg	tgt	aca	aga	gaa	aag	cca	gat	ttc	tgc	ttt	ttg	gaa	634
Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu	
		75					80					85				
gaa	gat	cct	gga	ata	tgt	cga	ggt	tat	att	acc	agg	tat	ttt	tat	aac	682
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn	
	90					95					100					
aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggt	gga	tgc	ctg	ggc	730
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly	
105				110					115						120	
aat	atg	aac	aat	ttt	gag	aca	ctg	gaa	gaa	tgc	aag	aac	att	tgt	gaa	778
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu	
				125				130					135			
gat	ggt	ccg	aat	ggt	ttc	cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat	826
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn	
			140					145				150				
gct	gtg	aat	aac	tcc	ctg	act	ccg	caa	tca	acc	aag	gtt	ccc	agc	ctt	874
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu	
		155				160					165					
ttt	gaa	ttt	cac	ggt	ccc	tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga	922
Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly	
	170			175					180							
ttg	tgt	cgt	gcc	aat	gag	aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg	970
Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly	
185				190					195						200	
aaa	tgc	cgc	cca	ttt	aag	tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat	1018
Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn	
			205					210				215				
ttt	act	tcc	aaa	caa	gaa	tgt	ctg	agg	gca	tgt	aaa	aaa	ggt	ttc	atc	1066
Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile	

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 Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys  
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 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu  
 40 45 50  
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser  
 55 60 65  
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys  
 70 75 80  
 Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr  
 85 90 95 100  
 Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly  
 105 110 115  
 Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn  
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 Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val  
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 Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala  
 165 170 175 180  
 Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser  
 185 190 195  
 Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn  
 200 205 210  
 Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys  
 215 220 225  
 Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg  
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Met His Phe Cys Gly Gly Thr Leu Ile Ser
1 5 10
cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc cca agg 1121
Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg
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cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc 1169
Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu
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gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg gag ccc 1217
Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro
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Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val Ile
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Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr Val Val
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Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly
95 100 105
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Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val Ile Glu
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125 130 135
acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag 1505
Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln
140 145 150
ggg gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa tac att 1553
Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile
155 160 165 170
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Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys
175 180 185
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Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly
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Val Met Arg Asn Asn
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 Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala  
 50 55 60  
 Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro  
 65 70 75 80  
 Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys  
 85 90 95  
 Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu  
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 115 120 125  
 Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly  
 130 135 140  
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 agaaagggtgt ggttggcatg gggca atg ctt gag gta tca gat gca ctg gga 52  
 Met Leu Glu Val Ser Asp Ala Leu Gly  
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 gga cct gga aga gta cca ggg gcc aca gca ggg atg aat gga gtg gac 100

Gly Pro Gly Arg Val Pro Gly Ala Thr Ala Gly Met Asn Gly Val Asp  
 10 15 20 25  
 acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga 148  
 Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg  
 30 35 40  
 aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct 196  
 Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro  
 45 50 55  
 ggg aag tac tac aag gag gca acg ctc acc atg gac cag gtc agc tcc 244  
 Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser  
 60 65 70  
 ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg 292  
 Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val  
 75 80 85  
 ttc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca 340  
 Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala  
 90 95 100 105  
 tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc 388  
 Ser Val Phe Ser Glu Gln Ala Cys Pro Ser Leu Lys Ile Glu Tyr Ala  
 110 115 120  
 ttt cgc atc tat gat ttt aat gag aat ggc ttc att gat gag gag gat 436  
 Phe Arg Ile Tyr Asp Phe Asn Glu Asn Gly Phe Ile Asp Glu Glu Asp  
 125 130 135  
 ctg cag agg atc atc ctg cga ctg ctg aac agt gat gac atg tct gag 484  
 Leu Gln Arg Ile Ile Leu Arg Leu Leu Asn Ser Asp Asp Met Ser Glu  
 140 145 150  
 gac ctc ctg atg gac ctc acg aac cac gtc ctg agt gag tgc gat ctg 532  
 Asp Leu Leu Met Asp Leu Thr Asn His Val Leu Ser Glu Ser Asp Leu  
 155 160 165  
 gac aat gac aac atg ctg tcc ttc tca gag ttt gaa cat gca atg gcc 580  
 Asp Asn Asp Asn Met Leu Ser Phe Ser Glu Phe Glu His Ala Met Ala  
 170 175 180 185  
 aag tct cca gat ttc atg aac tcc ttt cgg att cac ttc tgg gga tgc 628  
 Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys  
 190 195 200  
 tgatgtagcg gcaaatacct gacatggcag cctcgaggga gaccacagga atcgaaacccc 688  
 ctccagcact ggagggagct ggtttgaagt atgactttgt actggggccca cactcacctc 748  
 tagaatattg tttattagat aaaagaaaaa gcttttcctt agcccgaaaa aaaaaaaaaa 808  
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 <211> 201  
 <212> PRT  
 <213> Homo sapiens

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 Leu Gln Ala Leu Thr Phe Leu Thr Arg Asn Glu Ile Leu Cys Ile His  
 35 40 45  
 Asp Thr Phe Leu Lys Leu Cys Pro Pro Gly Lys Tyr Tyr Lys Glu Ala  
 50 55 60  
 Thr Leu Thr Met Asp Gln Val Ser Ser Leu Pro Ala Leu Arg Val Asn  
 65 70 75 80  
 Pro Phe Arg Asp Arg Ile Cys Arg Val Phe Ser His Lys Gly Met Phe  
 85 90 95  
 Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala  
 100 105 110  
 Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn  
 115 120 125  
 Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg



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      85      90      95
cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
      100      105      110
ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
      115      120      125
cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
      130      135      140      145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
      150      155      160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
Phe Gly
ccaaagctta taggactctg tgacaggttg tgaatgtttt ttttggtgtt gttgttggtt 1074
ttaattgctg ttaatatattt ttaaataata aagaaacaaa actaaaaaaaa aaaaaaaaa 1133

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<210> 58
<211> 163
<212> PRT
<213> Homo sapiens

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<400> 58
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      20      25      30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
      35      40      45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
      50      55      60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
      65      70      75      80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
      85      90      95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
      100      105      110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
      115      120      125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
      130      135      140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
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Pro Phe Gly

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<210> 59
<211> 838
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<220>
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Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
      100              105              110
ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc   608
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
      115              120              125              130
cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat   656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
      135              140              145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc   704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
      150              155              160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag   752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
      165              170              175
ttc ggg atc gtg tagccggcgg ggcggggggcc gtgggggggcc tggaggaggg   804
Phe Gly Ile Val
      180
caggagccgc gggaggccgg gaggagggtg gggaccttgc agcccccatc ctctccgt   862

<210> 62
<211> 202
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..21

<400> 62
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Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
      -5              1              5              10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
      15              20              25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
      30              35              40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
      45              50              55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
      60              65              70              75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
      80              85              90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
      95              100              105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
      110              115              120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
      125              130              135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
      140              145              150              155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
      160              165              170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
      175              180

<210> 63
<211> 618
<212> DNA
<213> Homo sapiens
  
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 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120  
 ttcgtttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180  
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu  
 -20 -15 -10  
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278  
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala  
 -5 1 5  
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326  
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln  
 10 15 20  
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374  
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala  
 25 30 35  
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422  
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr  
 40 45 50 55  
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470  
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser  
 60 65 70  
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518  
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg  
 75 80 85  
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566  
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met  
 90 95 100  
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618  
 Cys Phe Ala Leu Leu Asn Cys  
 105 110

<210> 64  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..22

<400> 64  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly





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Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
      80      85      90
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
      95     100     105
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct 611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
     110     115     120
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc 659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
    125     130     135     140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc 707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
      145     150     155
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt 755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
      160     165     170
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg 807
Phe Ser Pro Ala
     175
atagtgtata aatgaaaaaa aaaaaaaaaa 836

<210> 66
<211> 197
<212> PRT
<213> Homo sapiens

<220>
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<222> 1..22

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Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
      -5       1       5      10
Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
      15      20      25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
      30      35      40
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
      45      50      55
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
      60      65      70
Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
      75      80      85      90
Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
      95     100     105
Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
     110     115     120
Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp
     125     130     135
Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
     140     145     150
Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
    155     160     165     170
Leu Phe Ser Pro Ala
      175

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<210> 67

<211> 789  
 <212> DNA  
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 <222> 750..755

<220>  
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 <222> 774..789

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 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107  
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly  
 1 5 10 15  
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155  
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys  
 20 25 30  
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203  
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu  
 35 40 45  
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251  
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu  
 50 55 60  
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299  
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro  
 65 70 75  
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347  
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val  
 80 85 90 95  
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395  
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu  
 100 105 110  
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443  
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile  
 115 120 125  
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491  
 Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr  
 130 135 140  
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539  
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro  
 145 150 155  
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592  
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
 160 165 170  
 gaggagggac gcccaggggt gggaggaaga gtctgcaagc agggctgtgg agttaggggt 652  
 caccaccaatg ggaccacct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712  
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 gaaaaaaaa aaaaaaa 789

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 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
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 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu  
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 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu  
 35 40 45  
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val  
 50 55 60  
 Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu  
 65 70 75 80  
 Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu  
 85 90 95  
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu  
 100 105 110  
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn  
 115 120 125  
 Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val  
 130 135 140  
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val  
 145 150 155 160  
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
 165 170

<210> 69  
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 <212> DNA  
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 <222> 2428..2556

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 <222> 2522..2527

<220>  
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 <222> 2541..2556

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 Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu  
 -15 -10 -5  
 ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156  
 Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile  
 1 5 10 15

cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat	204
Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr	
20 25 30	
gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg	252
Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val	
35 40 45	
cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg	300
His Leu Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu	
50 55 60	
tac aat caa gga tct atg aat act tat tct tca gat att cag act caa	348
Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln	
65 70 75	
tgc tac tat caa gga aat att gaa gaa tat cca gat tcc atg gtc aca	396
Cys Tyr Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr	
80 85 90 95	
ctc agc acg tgc tct gga cta aga gga ata ctg caa ttt gaa aat gtt	444
Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val	
100 105 110	
tct tat gga att gag cct ctg gaa tct gca gtt gaa ttt cag cat gtt	492
Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val	
115 120 125	
ctt cac aaa tta aag aat gaa gac aat gat att gca att ttt att gac	540
Leu His Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp	
130 135 140	
aga agc ctg aaa gaa caa cca atg gat gac aac att ttt ata agt gaa	588
Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu	
145 150 155	
aaa tca gaa cca gct gtt cca gat tta ttt cct ctt tat cta gaa atg	636
Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met	
160 165 170 175	
cat att gtg gtg gac aaa act ttg tat gat tac tgg ggc tct gat agc	684
His Ile Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser	
180 185 190	
atg ata gta aca aat aaa gtc atc gaa att gtt ggc ctt gca aat tca	732
Met Ile Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser	
195 200 205	
atg ttc acc caa ttt aaa gtt act att gtg ctg tca tca ttg gag tta	780
Met Phe Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu	
210 215 220	
tgg tca gat gaa aat aag att tct aca gtt ggt gag gca gat gaa tta	828
Trp Ser Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu	
225 230 235	
ttg caa aaa ttt tta gaa tgg aaa caa tct tat ctt aac cta agg cct	876
Leu Gln Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro	
240 245 250 255	
cat gat att gca tat cta cta att tat atg gat tat cct cgt tat ttg	924
His Asp Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu	
260 265 270	
gga gca gtg ttt cct gga aca atg tgt att act cgt tat tct gca gga	972
Gly Ala Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly	
275 280 285	
gtc gca ttg tac ccc aag gag ata act ctg gag gca ttt gca gtt att	1020
Val Ala Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile	
290 295 300	
gtc acc cag atg ctg gca ctc agt ctg gga ata tca tat gac gac cca	1068
Val Thr Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro	
305 310 315	
aag aaa tgt caa tgt tca gaa tcc acc tgt ata atg aat cca gaa gtt	1116
Lys Lys Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val	
320 325 330 335	
gtg caa tcc aat ggt gtg aag act ttt agc agt tgc agt ttg agg agc	1164
Val Gln Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser	
340 345 350	

ttt	caa	aat	ttc	att	tca	aat	gtg	ggt	gtc	aaa	tgt	ctt	cag	aat	aag	1212
Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
			355				360						365			
cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
			370				375						380			
ttg	gag	gga	aat	gaa	atc	tgt	gat	tgt	ggg	act	gag	gct	caa	tgt	gga	1308
Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly	
			385				390						395			
cct	gca	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	ctg	aaa	gac	gga	gca	1356
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	
			400				405						410			415
aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser	
			420							425			430			
ggc	gtt	gaa	tgt	agg	ccg	aaa	gca	cat	cct	gaa	tgt	gac	atc	gct	gaa	1452
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	
			435				440						445			
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggg	cct	gac	ata	act	tta	atc	1500
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	
			450				455						460			
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	
			465				470						475			
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggg	tca	1596
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	
			480				485						490			495
aga	aat	gct	cca	ttt	gcc	tgc	tat	gaa	gaa	ata	caa	tct	caa	tca	gac	1644
Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	
			500				505						510			
aga	ttt	ggg	aac	tgt	ggg	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys	
			515				520						525			
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	gtt	tgt	acc	tac	cct	act	1740
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	
			530				535						540			
cga	aag	cct	ttc	cat	caa	gaa	aat	ggt	gat	gtg	att	tat	gct	ttc	gta	1788
Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	
			545				550						555			
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	gtt	1836
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	
			560				565						570			575
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884
Pro	Asp	Pro	Leu	Ala</												

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gca agg aaa cag ttg aaa aac tgg ttc gcc aag gaa gag gaa ttc cca 2220
Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro
      690                695                700
agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa 2268
Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln
      705                710                715
tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca 2316
Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
      720                725                730                735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
      740                745                750
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
      755                760                765
caa agc agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
Gln Ser Ser Ser Asn
      770
tcgctaagaa atgaaaattc tgtctttcct tccgtgggtca cagctgaaag aaacaataaa 2527
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<212> PRT
<213> Homo sapiens

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<221> SIGNAL
<222> 1..16

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  1      5      10      15
Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
  20      25      30
Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
  35      40      45
Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
  50      55      60
Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
  65      70      75      80
Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
  85      90      95
Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
  100     105     110
Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
  115     120     125
Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
  130     135     140
Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
  145     150     155     160
Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
  165     170     175
Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
  180     185     190
Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
  195     200     205
Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
  210     215     220
Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
  225     230     235     240

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Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp  
245 250 255  
Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala  
260 265 270  
Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala  
275 280 285  
Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr  
290 295 300  
Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys  
305 310 315 320  
Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln  
325 330 335  
Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln  
340 345 350  
Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln  
355 360 365  
Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu  
370 375 380  
Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala  
385 390 395 400  
Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys  
405 410 415  
Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val  
420 425 430  
Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys  
435 440 445  
Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly  
450 455 460  
Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His  
465 470 475 480  
Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn  
485 490 495  
Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe  
500 505 510  
Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp  
515 520 525  
Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys  
530 535 540  
Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp  
545 550 555 560  
Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp  
565 570 575  
Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys  
580 585 590  
Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His  
595 600 605  
Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn  
610 615 620  
Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg  
625 630 635 640  
Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met  
645 650 655  
Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu  
660 665 670  
Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg  
675 680 685  
Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser  
690 695 700  
Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser  
705 710 715 720  
Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser  
725 730 735  
Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu



740                      745                      750  
 Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser  
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 Ser Ser Asn  
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 <212> DNA  
 <213> Homo sapiens

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<220>  
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<220>  
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 <222> 1588..1603

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                     -15                      -10                      -5  
 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97  
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro  
           1                                      5                                      10  
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145  
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu  
           15                                      20                                      25                                      30  
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193  
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile  
                     35                                      40                                      45  
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241  
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val  
                     50                                      55                                      60  
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289  
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu  
           65                                      70                                      75  
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337  
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu  
           80                                      85                                      90  
 tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat 385  
 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Leu Ser Met Phe His  
           95                                      100                                      105                                      110  
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433  
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile  
                     115                                      120                                      125  
 ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481  
 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val  
                     130                                      135                                      140  
 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529

Leu	Val	Ala	Leu	Gly	Pro	Gly	His	Gly	Leu	Gln	Gly	Pro	His	Xaa	Ala		
		145					150					155					
ctc	ctg	gct	gca	atg	ctt	cgg	ggg	ctg	gca	ggg	ggc	cga	gtc	ctg	gcc	577	
Leu	Leu	Ala	Ala	Met	Leu	Arg	Gly	Leu	Ala	Gly	Gly	Arg	Val	Leu	Ala		
		160				165					170						
ctc	ctg	gag	gag	aac	tcc	aca	ccc	cag	cta	gca	ggg	atc	ctg	gcc	cgg	625	
Leu	Leu	Glu	Glu	Asn	Ser	Thr	Pro	Gln	Leu	Ala	Gly	Ile	Leu	Ala	Arg		
		175			180					185				190			
gtg	ctg	aat	gga	gag	gca	cct	cct	agc	cta	ggc	cct	tcc	tct	gtg	gcc	673	
Val	Leu	Asn	Gly	Glu	Ala	Pro	Pro	Ser	Leu	Gly	Pro	Ser	Ser	Val	Ala		
			195						200					205			
tcc	cca	gag	gac	gtc	cag	gcc	ctg	atg	tac	ctg	aga	ggg	cag	ctg	gag	721	
Ser	Pro	Glu	Asp	Val	Gln	Ala	Leu	Met	Tyr	Leu	Arg	Gly	Gln	Leu	Glu		
		210						215				220					
cct	cag	tgg	aag	atg	ttg	cag	tgc	cat	cct	cac	ctg	gtg	gct			763	
Pro	Gln	Trp	Lys	Met	Leu	Gln	Cys	His	Pro	His	Leu	Val	Ala				
		225				230					235						
tgaaatcggc	caaggtggga	gcatttacac	cgagaaatg	acaccgcacg	ccagcgcccc	823											
gcgccgcgca	tccggacccc	aagcccacgg	ctccctcgac	tctggggcac	ggaaccccg	883											
ccactcccaa	tccccgcgcc	ccgccctctc	ccaccctg	ttcccccgct	ccaccctca	943											
cctcacctcg	ccccgcgcc	acccatcgcg	ccccggcg	tggtattgtt	cggctgggct	1003											
cggtcggggc	gtgtctccct	cggctctg	ggtgtcagtt	cgtccggctt	cctcacagcc	1063											
cctcactccc	ggcggtgac	agcagcagcg	gcggcgcg	gcggcgctg	gcgtttcgag	1123											
gctgagcggc	accgggggtt	gggcgcggag	gaggagcagc	agcgggagga	ggagccgtgt	1183											
gccctggcac	tgagcggccg	cggccatggc	gtacgcctat	ctcttcaagt	acatcataat	1243											
cggcgacaca	ggtgttggt	aatcatgctt	attgctacag	tttacagaca	agaggttcag	1303											
ccagtgcatt	accttactat	tgggtgtagag	ttcgggtgctc	gaatgataac	tattgatggg	1363											
aaacagataa	aacttcagat	atgggatacg	gcagggcaag	aatcctttcg	ttccatcaca	1423											
aggtcgtatt	acagaggtgc	agcaggagct	ttactagttt	acgatattac	acggagagat	1483											
acattcaacc	acttgacaac	ctgggttagaa	gatgcccgcc	agcattccaa	ttccaacatg	1543											
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<210> 72  
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 1..17

<220>  
 <221> UNSURE  
 <222> 173  
 <223> Xaa = Ala,Gly

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Leu	Arg	Val	Cys	Val	Ser	Leu	Trp	Ser	Val	His	Arg	Pro	His	Glu			
	1			5					10					15			
Ser	Leu	Ala	Arg	Glu	Ala	Leu	Thr	Ala	Leu	Gly	Lys	Leu	Leu	Tyr			
			20					25					30				
Leu	Leu	Asp	Gly	Met	Leu	Asp	Gly	Gln	Val	Asn	Ser	Gly	Ile	Ala	Ala		
		35					40					45					
Thr	Pro	Ala	Ser	Ala	Ala	Ala	Ala	Thr	Leu	Asp	Val	Ala	Val	Arg	Arg		
	50					55					60						
Gly	Leu	Ser	His	Ala	Ala	Gln	Arg	Leu	Leu	Cys	Val	Ala	Leu	Gly	Gln		
	65				70					75							
Leu	Asp	Arg	Pro	Pro	Asp	Leu	Ala	His	Asp	Gly	Arg	Ser	Leu	Trp	Leu		
	80				85				90					95			
Asn	Ile	Arg	Gly	Lys	Glu	Ala	Ala	Ala	Leu	Ser	Met	Phe	His	Val	Ser		
			100					105						110			

Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile Leu Gly  
115 120 125  
Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val Leu Val  
130 135 140  
Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala Leu Leu  
145 150 155  
Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala Leu Leu  
160 165 170 175  
Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg Val Leu  
180 185 190  
Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala Ser Pro  
195 200 205  
Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu Pro Gln  
210 215 220  
Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala  
225 230 235

<210> 73  
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<212> DNA  
<213> Homo sapiens

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<222> 9..395

<220>  
<221> 3'UTR  
<222> 396..879

<220>  
<221> polyA\_site  
<222> 864..879

<400> 73  
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-15 -10 -5  
cca ggc ccg ggt cct cgg ccg ctg tgg ggc cca ggc ccg gcc tgg agt 98  
Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser  
1 5 10 15  
cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146  
Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser  
20 25 30  
agg cct ccg ggg gac ctc gcc gag gct gga ggc cga gct ctg cag agc 194  
Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser  
35 40 45  
tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242  
Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu  
50 55 60  
ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt 290  
Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu  
65 70 75  
tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat 338  
Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn  
80 85 90 95  
aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt 386  
Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly  
100 105 110

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ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac 435
Ile Phe Ile
rtttctgttt wccttttagc aaggtgaaac cagtctggam aatggggaga tgggccgggt 495
gcagtggctc acacttgtaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga 555
ggcctatacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtggtggc 615
tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacct gcaccctggc 675
caacatggtg aaaccccgtc ttactaaaa atagaaaatt agccgggcgt gatggcacac 735
gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggaggtg 795
gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaaac 855
tccatcccaa aaaaaaaaaa aaaa 879

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<210> 74
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..16

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<400> 74
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-15 -10 -5
Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
1 5 10 15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
20 25 30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
35 40 45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
50 55 60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
65 70 75 80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
85 90 95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
100 105 110
Ile

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<210> 75
<211> 1634
<212> DNA
<213> Homo sapiens

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<220>
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<222> 1..87

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<220>
<221> CDS
<222> 88..1269

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<220>
<221> 3'UTR
<222> 1270..1634

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<220>
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<222> 1594..1599

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<220>
<221> polyA_site
<222> 1619..1634

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<400> 75
aaagttcttc agcccttggc tcctgcccag tgttttagggg gttggcggag acaaagggga 60
agagtcacgc cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
Met Met Gly Val Phe Val Val Ala Ala
1 5
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162
Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr
10 15 20 25
gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210
Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly
30 35 40
aaa gtc tca cct gaa aca gtt gac agt gtg att atg ggc aat gtc ctg 258
Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu
45 50 55
cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306
Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg
60 65 70
gtg gga atc cca aag gag acc cca gct ctc acg att aat agg ctc tgt 354
Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys
75 80 85
ggg tct ggt ttt cag tcc att gtg aat gga tgt cag gaa att tgt gtt 402
Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val
90 95 100 105
aaa gaa gct gaa gtt gtt tta tgt gga gga acc gaa agc atg agc caa 450
Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln
110 115 120
gct ccc tac tgt gtc aga aat gtg cgt ttt gga acc aag ctt gga tca 498
Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser
125 130 135
gat atc aag ctg gaa gat tct tta tgg gta tca tta aca gat cag cat 546
Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His
140 145 150
gtc cag ctc ccc atg gca atg act gca gag aat ctt gct gta aaa cac 594
Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn Leu Ala Val Lys His
155 160 165
aaa ata agc aga gaa gaa tgt gac aaa tat gcc ctg cag tca cag cag 642
Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln
170 175 180 185
aga tgg aaa gct gct aat gat gct ggc tac ttt aat gat gaa atg gca 690
Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala
190 195 200
cca att gaa gtg aag aca aag aaa gga aaa cag aca atg cag gta gac 738
Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp
205 210 215
gag cat gct cgg ccc caa acc acc ctg gaa cag tta cag aaa ctt cct 786
Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro
220 225 230
cca gta ttc aag aaa gat gga act gtt act gca ggg aat gca tcg ggt 834
Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly
235 240 245
gta gct gat ggt gct gga gct gtt atc ata gct agt gaa gat gct gtt 882
Val Ala Asp Gly Ala Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val
250 255 260 265
aag aaa cat aac ttc aca cca ctg gca aga att gtg ggc tac ttt gta 930
Lys Lys His Asn Phe Thr Pro Leu Ala Arg Ile Val Gly Tyr Phe Val
270 275 280
tct gga tgt gat ccc tct atc atg ggt att ggt cct gtc cct gct atc 978
Ser Gly Cys Asp Pro Ser Ile Met Gly Ile Gly Pro Val Pro Ala Ile
285 290 295
agt ggg gca ctg aag aaa gca gga ctg agt ctt aag gac atg gat ttg 1026
Ser Gly Ala Leu Lys Lys Ala Gly Leu Ser Leu Lys Asp Met Asp Leu
300 305 310

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gta gag gtg aat gaa gct ttt gct ccc cag tac ttg gct gtt gag agg 1074
Val Glu Val Asn Glu Ala Phe Ala Pro Gln Tyr Leu Ala Val Glu Arg
    315                320                325
agt ttg gat ctt gac ata agt aaa acc aat gtg aat gga gga gcc att 1122
Ser Leu Asp Leu Asp Ile Ser Lys Thr Asn Val Asn Gly Gly Ala Ile
    330                335                340                345
gct ttg ggt cac cca ctg gga gga tct gga tca aga att act gca cac 1170
Ala Leu Gly His Pro Leu Gly Gly Ser Gly Ser Arg Ile Thr Ala His
                350                355                360
ctg gtt cac gaa tta agg cgt cga ggt gga aaa tat gcc gtt gga tca 1218
Leu Val His Glu Leu Arg Arg Arg Gly Gly Lys Tyr Ala Val Gly Ser
                365                370                375
gct tgc att gga ggt ggc caa ggt att gct gtc atc att cag agc aca 1266
Ala Cys Ile Gly Gly Gly Gln Gly Ile Ala Val Ile Ile Gln Ser Thr
    380                385                390
gcc tgaagagacc agtgagctca ctgtgaccca tccttactct acttggccag 1319
Ala
gccacagtaa aacaagtgac cttcagagca gctgccacaa ctggccatgc cctgccattg 1379
aaacagtgat taagtttgat caagccatgg tgacacaaaa atgcattgat catgaatagg 1439
agcccatgct agaagtacat tctctcagat ttgaaccagt gaaatatgat gtatttctga 1499
gctaaaactc aactatagaa gacattaaaa gaaatcgtat tcttgccaag taaccaccac 1559
ttctgcctta gataatatga ttataaggaa atcaaataaa tgttgccctta acttcaaaca 1619
aaaaaaaaaa aaaaaa 1634

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<210> 76  
 <211> 394  
 <212> PRT  
 <213> Homo sapiens

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Tyr Gly Gly Leu Leu Lys Asp Phe Thr Ala Thr Asp Leu Ser Glu Phe
    20          25          30
Ala Ala Lys Ala Ala Leu Ser Ala Gly Lys Val Ser Pro Glu Thr Val
    35          40          45
Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile
    50          55          60
Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr
65          70          75          80
Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile
    85          90          95
Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu
    100         105         110
Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn
    115         120         125
Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser
    130         135         140
Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met
145         150         155         160
Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys
    165         170         175
Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp
    180         185         190
Ala Gly Tyr Phe Asn Asp Glu Met Ala Pro Ile Glu Val Lys Thr Lys
    195         200         205
Lys Gly Lys Gln Thr Met Gln Val Asp Glu His Ala Arg Pro Gln Thr
    210         215         220
Thr Leu Glu Gln Leu Gln Lys Leu Pro Pro Val Phe Lys Lys Asp Gly
225         230         235         240
Thr Val Thr Ala Gly Asn Ala Ser Gly Val Ala Asp Gly Ala Gly Ala
    245         250         255
Val Ile Ile Ala Ser Glu Asp Ala Val Lys Lys His Asn Phe Thr Pro

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ggc	acg	gcc	aac	atc	cag	ctc	cac	ggg	cct	ccc	aga	gtg	aag	gcc	gtg	398
Gly	Thr	Ala	Asn	Ile	Gln	Leu	His	Gly	Pro	Pro	Arg	Val	Lys	Ala	Val	
75					80					85					90	
aag	tcg	tca	gaa	cac	atc	aac	gag	ggg	gag	acg	gcc	atg	ctg	gtc	tgc	446
Lys	Ser	Ser	Glu	His	Ile	Asn	Glu	Gly	Glu	Thr	Ala	Met	Leu	Val	Cys	
			95					100						105		
aag	tca	gag	tcc	gtg	cca	cct	gtc	act	gac	tgg	gcc	tgg	tac	aag	atc	494
Lys	Ser	Glu	Ser	Val	Pro	Pro	Val	Thr	Asp	Trp	Ala	Trp	Tyr	Lys	Ile	
			110					115					120			
act	gac	tct	gag	gac	aag	gcc	ctc	atg	aac	ggc	tcc	gag	agc	agg	ttc	542
Thr	Asp	Ser	Glu	Asp	Lys	Ala	Leu	Met	Asn	Gly	Ser	Glu	Ser	Arg	Phe	
		125					130					135				
ttc	gtg	agt	tcc	tcg	cag	ggc	ctg	tca	gag	cta	cac	att	gag	aac	ctg	590
Phe	Val	Ser	Ser	Ser	Gln	Gly	Leu	Ser	Glu	Leu	His	Ile	Glu	Asn	Leu	
	140					145					150					
aac	atg	gag	gcc	gac	ccc	ggc	cag	tac	cgg	tgc	aac	ggc	acc	agc	tcc	638
Asn	Met	Glu	Ala	Asp	Pro	Gly	Gln	Tyr	Arg	Cys	Asn	Gly	Thr	Ser	Ser	
155					160					165					170	
aag	ggc	tcc	gac	cag	gcc	atc	atc	acg	ctc	cgc	gtg	cgc	agc	cac	ctg	686
Lys	Gly	Ser	Asp	Gln	Ala	Ile	Ile	Thr	Leu	Arg	Val	Arg	Ser	His	Leu	
			175					180					185			
gcc	gcc	ctc	tgg	ccc	ttc	ctg	ggc	atc	gtg	gct	gag	gtg	ctg	gtg	ctg	734
Ala	Ala	Leu	Trp	Pro	Phe	Leu	Gly	Ile	Val	Ala	Glu	Val	Leu	Val	Leu	
			190					195					200			
gtc	acc	atc	atc	ttc	atc	tac	gag	aag	cgc	cgg	aag	ccc	gag	gac	gtc	782
Val	Thr	Ile	Ile	Phe	Ile	Tyr	Glu	Lys	Arg	Arg	Lys	Pro	Glu	Asp	Val	
		205					210					215				
ctg	gat	gat	gac	gac	gcc	ggc	tct	gca	ccc	ctg	aag	agc	agc	ggg	cag	830
Leu	Asp	Asp	Asp	Asp	Ala	Gly	Ser	Ala	Pro	Leu	Lys	Ser	Ser	Gly	Gln	
	220					225					230					
cac	cag	aat	gac	aaa	ggc	aag	aac	gtc	cgc	cag	agg	aac	tct	tcc		875
His	Gln	Asn	Asp	Lys	Gly	Lys	Asn	Val	Arg	Gln	Arg	Asn	Ser	Ser		
235					240					245						
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ccagtgctt			gcaagattcc			aagttctcac		ctcttaaaga			aaacccaccc		cgtagattcc			995
catcatacac			ttccttcttt			tttaaaaaag		ttgggttttc			tccatttcagg		attctgttcc			1055
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cgtctgtggc			tttcagcctc			tgggtctgag		tcatggccgg			gtgggcggca		cagccttctc			1175
actgtggccg			agtcagtgcc			aggctcctgc		cctttgtgga			aagtcacagg		tcacacgagg			1235
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<210> 78
<211> 269
<212> PRT
<213> Homo sapiens
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Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu  
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 Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp  
 45 50 55  
 Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr  
 60 65 70 75  
 Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser  
 80 85 90  
 Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser  
 95 100 105  
 Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp  
 110 115 120  
 Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val  
 125 130 135  
 Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met  
 140 145 150 155  
 Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly  
 160 165 170  
 Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala  
 175 180 185  
 Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr  
 190 195 200  
 Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp  
 205 210 215  
 Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln  
 220 225 230 235  
 Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser  
 240 245

<210> 79  
 <211> 1466  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..343

<220>  
 <221> CDS  
 <222> 344..1144

<220>  
 <221> 3'UTR  
 <222> 1145..1466

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 aattggcagc cttagaacta gtgggaaggc ggggtgcgcga agtcgagggg cggagagagg 120  
 gggccggagg agctgctttc tgaatccaag ttctgtgggct ctctcagaag tcctcaggac 180  
 ggagcagagg tggccggcgg gcccggtga ctgcgcctyt gctttctttc cataaccttt 240  
 tctttcggac tcgaatcacg gctgctgcga agggcttagt tccggacact aggggtgcccg 300  
 aacgcgctga tgccccgagt gctcgcaggg cttcccgccta acc atg ctg ccg ccg 355  
 Met Leu Pro Pro  
 ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg 403  
 Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu  
 -25 -20 -15 -10  
 gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca 451  
 Val Val Leu Thr Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro  
 -5 1 5  
 gat tac ctg cgg cgc ggc tgg atg ccg ctg cta gcg gag ggc gag ggc 499  
 Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly  
 10 15 20

tgc	gct	ccc	tgc	cgg	cca	gaa	gag	tgc	gcc	gcg	ccg	cgg	ggc	tgc	ctg	547
Cys	Ala	Pro	Cys	Arg	Pro	Glu	Glu	Cys	Ala	Ala	Pro	Arg	Gly	Cys	Leu	
25						30					35					
gcg	ggc	agg	gtg	cgc	gac	gcg	tgc	ggc	tgc	tgc	tgg	gaa	tgc	gcc	aac	595
Ala	Gly	Arg	Val	Arg	Asp	Ala	Cys	Gly	Cys	Cys	Trp	Glu	Cys	Ala	Asn	
40					45					50					55	
ctc	gag	ggc	cag	ctc	tgc	gac	ctg	gac	ccc	agt	gct	cac	ttc	tac	ggg	643
Leu	Glu	Gly	Gln	Leu	Cys	Asp	Leu	Asp	Pro	Ser	Ala	His	Phe	Tyr	Gly	
				60					65					70		
cac	tgc	ggc	gag	cag	ctt	gag	tgc	cgg	ctg	gac	aca	ggc	ggc	gac	ctg	691
His	Cys	Gly	Glu	Gln	Leu	Glu	Cys	Arg	Leu	Asp	Thr	Gly	Gly	Asp	Leu	
				75				80					85			
agc	cgc	gga	gag	gtg	ccg	gaa	cct	ctg	tgt	gcc	tgt	cgt	tcg	cag	agt	739
Ser	Arg	Gly	Glu	Val	Pro	Glu	Pro	Leu	Cys	Ala	Cys	Arg	Ser	Gln	Ser	
		90					95					100				
ccg	ctc	tgc	ggg	tcc	gac	ggt	cac	acc	tac	tcc	cag	atc	tgc	cgc	ctg	787
Pro	Leu	Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Gln	Ile	Cys	Arg	Leu	
						110					115					
cag	gag	gcg	gcc	cgc	gct	cgg	ccc	gat	gcc	aac	ctc	act	gtg	gca	cac	835
Gln	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Asp	Ala	Asn	Leu	Thr	Val	Ala	His	
120					125					130					135	
ccg	ggg	ccc	tgc	gaa	tcg	ggg	ccc	cag	atc	gtg	tca	cat	cca	tat	gac	883
Pro	Gly	Pro	Cys	Glu	Ser	Gly	Pro	Gln	Ile	Val	Ser	His	Pro	Tyr	Asp	
				140					145					150		
act	tgg	aat	gtg	aca	ggg	cag	gat	gtg	atc	ttt	ggc	tgt	gaa	gtg	ttt	931
Thr	Trp	Asn	Val	Thr	Gly	Gln	Asp	Val	Ile	Phe	Gly	Cys	Glu	Val	Phe	
				155				160					165			
gcc	tac	ccc	atg	gcc	tcc	atc	gag	tgg	agg	aag	gat	ggc	ttg	gac	atc	979
Ala	Tyr	Pro	Met	Ala	Ser	Ile	Glu	Trp	Arg	Lys	Asp	Gly	Leu	Asp	Ile	
		170					175					180				
cag	ctg	cca	ggg	gat	gac	ccc	cac	atc	tct	gtg	cag	ttt	agg	ggg	gga	1027
Gln	Leu	Pro	Gly	Asp	Asp	Pro	His	Ile	Ser	Val	Gln	Phe	Arg	Gly	Gly	
						190					195					
ccc	cag	agg	ttt	gag	gtg	act	ggc	tgg	ctg	cag	atc	cag	gct	gtg	cgt	1075
Pro	Gln	Arg	Phe	Glu	Val	Thr	Gly	Trp	Leu	Gln	Ile	Gln	Ala	Val	Arg	
200					205					210					215	
ccc	agt	gat	gag	ggc	act	tac	cgc	tgc	ctt	ggc	cca	atg	ccc	tgg	gtc	1123
Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Arg	Cys	Leu	Gly	Pro	Met	Pro	Trp	Val	
				220					225					230		
aag	tgg	agg	ccc	ctg	cta	gct	tgacagt	gct	cacacct	gac	cagctga	aact				1174

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<210> 80
<211> 267
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> 1..30
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<400> 80  
Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu  
-30 -25 -20 -15  
Leu Leu Leu Leu Val Leu Thr Pro Pro Thr Gly Ala Arg Pro  
-10 -5 1  
Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala



Ile	Leu	Ser	Gly	Gly	Glu	Ser	Thr	Glu	Ile	Pro	Pro	Tyr	Val	Met	Lys	
-5						1				5					10	
tgt	ccg	agc	aat	ggg	ttg	tgt	agc	agg	ctt	cct	gca	gac	tgt	ata	gac	197
Cys	Pro	Ser	Asn	Gly	Leu	Cys	Ser	Arg	Leu	Pro	Ala	Asp	Cys	Ile	Asp	
			15					20						25		
tgc	aca	aca	aat	ttc	tcc	tgt	acc	tat	ggg	aag	cct	gtc	act	ttt	gac	245
Cys	Thr	Thr	Asn	Phe	Ser	Cys	Thr	Tyr	Gly	Lys	Pro	Val	Thr	Phe	Asp	
			30					35					40			
tgt	gca	gtg	aaa	cca	tct	gtt	acc	tgt	gtt	gat	caa	gac	ttc	aaa	tcc	293
Cys	Ala	Val	Lys	Pro	Ser	Val	Thr	Cys	Val	Asp	Gln	Asp	Phe	Lys	Ser	
			45				50					55				
caa	aag	aac	ttc	atc	att	aac	atg	act	tgc	aga	ttt	tgc	tgg	cag	ctt	341
Gln	Lys	Asn	Phe	Ile	Ile	Asn	Met	Thr	Cys	Arg	Phe	Cys	Trp	Gln	Leu	
			60			65						70				
cct	gaa	aca	gat	tac	gag	tgt	acc	aac	tcc	acc	agc	tgc	atg	acg	gtg	389
Pro	Glu	Thr	Asp	Tyr	Glu	Cys	Thr	Asn	Ser	Thr	Ser	Cys	Met	Thr	Val	
					80					85					90	
tcc	tgt	cct	cgg	cag	cgc	tac	cct	gcc	aac	tgc	acg	gtg	cgg	gac	cac	437
Ser	Cys	Pro	Arg	Gln	Arg	Tyr	Pro	Ala	Asn	Cys	Thr	Val	Arg	Asp	His	
			95					100						105		
gtc	cac	tgc	ttg	ggg	aac	cgt	act	ttt	ccc	aaa	atg	cta	tat	tgc	aat	485
Val	His	Cys	Leu	Gly	Asn	Arg	Thr	Phe	Pro	Lys	Met	Leu	Tyr	Cys	Asn	
			110					115					120			
tgg	act	gga	ggc	tat	aag	tgg	tct	acg	gct	ctg	gct	cta	agc	atc	acc	533
Trp	Thr	Gly	Gly	Tyr	Lys	Trp	Ser	Thr	Ala	Leu	Ala	Leu	Ser	Ile	Thr	
			125				130					135				
ctc	ggg	ggg	ttt	gga	gca	gac	cgt	ttc	tac	ctg	ggc	cag	tgg	cgg	gaa	581
Leu	Gly	Gly	Phe	Gly	Ala	Asp	Arg	Phe	Tyr	Leu	Gly	Gln	Trp	Arg	Glu	
			140				145					150				
ggc	ctc	ggc	aag	ctc	ttc	agc	ttc	ggg	ggc	ctg	gga	ata	tgg	acg	ctg	629
Gly	Leu	Gly	Lys	Leu	Phe	Ser	Phe	Gly	Gly	Leu	Gly	Ile	Trp	Thr	Leu	
					160					165					170	
ata	gac	gtc	ctg	ctc	att	gga	gtt	ggc	tat	gtt	gga	cca	gca	gat	ggc	677
Ile	Asp	Val	Leu	Leu	Ile	Gly	Val	Gly	Tyr	Val	Gly	Pro	Ala	Asp	Gly	
			175						180					185		
tct	ttg	tac	att	tagctgtggg	gtgtgcttca	gaaaggagca	gggcttagaa									729
Ser	Leu	Tyr	Ile													
			190													
aaagcccttt	tgtccgtagg	agttgatgtg	gtgtgagtga	tatatcttcta	tggttttaaat											789
gtacagcatc	tgtactttgt	ttgccttgat	aaaggtaaga	taaatgaaac	gctgaactat											849
gctaactctgg	aattttgtttt	tatttgccctg	aaatatattt	ttttctgtga	aaaa											

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<210> 82
<211> 221
<212> PRT
<213> Homo sapiens
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<400> 82  
Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg  
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Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser  
 -15 -10 -5  
 Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys  
 1 5 10 15  
 Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys  
 20 25 30  
 Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val  
 35 40 45  
 Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn  
 50 55 60  
 Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys  
 65 70 75 80  
 Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr  
 85 90 95  
 Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg  
 100 105 110  
 Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp  
 115 120 125  
 Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp  
 130 135 140  
 Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser  
 145 150 155 160  
 Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly  
 165 170 175  
 Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile  
 180 185

<210> 83  
 <211> 1754  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..117

<220>  
 <221> CDS  
 <222> 118..510

<220>  
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 <222> 511..1754

<220>  
 <221> polyA\_signal  
 <222> 1718..1723

<220>  
 <221> polyA\_site  
 <222> 1739..1754

<400> 83  
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 gcggttcgcc ccgcagctc gccccctgcc caccggggcg gccgtagggc gggtcacg 117  
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165  
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu  
 -20 -15 -10  
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213  
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
 -5 1 5  
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala

10									15									20									25	
ggg	cgg	cag	gcc	gag	ttg	tgc	cag	gct	gag	ccg	gaa	gtg	gtg	gca	gag	309												
Gly	Arg	Gln	Ala	Glu	Leu	Cys	Gln	Ala	Glu	Pro	Glu	Val	Val	Ala	Glu													
				30				35				40																
ctg	gct	cgg	ggc	gcc	cgg	ctc	ggg	gtg	cga	gag	tgc	cag	ttc	cag	ttc	357												
Leu	Ala	Arg	Gly	Ala	Arg	Leu	Gly	Val	Arg	Glu	Cys	Gln	Phe	Gln	Phe													
				45				50				55																
cgc	ttc	cgc	cgc	tgg	aat	tgc	tcc	agc	cac	agc	aag	gcc	ttt	gga	cgc	405												
Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg													
				60				65				70																
atc	ctg	caa	cag	ggg	cag	tgt	ggg	gag	ggg	cac	cct	gca	agg	acc	ctg	453												
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	His	Pro	Ala	Arg	Thr	Leu													
				75				80				85																
cct	ccc	agg	ccc	ctg	ggg	cag	ccc	tcc	cgc	cgc	agg	ttt	cag	gtc	cca	501												
Pro	Pro	Arg	Pro	Leu	Gly	Gln	Pro	Ser	Arg	Arg	Arg	Phe	Gln	Val	Pro													
				90				95				100				105												
ggc	ccc	agc	tgaccgcccc	agccccgcgct				gattgcacct				gtctgcattc				550												
Gly	Pro	Ser																										
acagacattc	gggagacggc				cttcgtgttc				gccatcactg				cggccggcgc				cagccacgcc	610										
gtcacgcagg	cctgttctat				gggcgagctg				ctgcagtgcg				gctgccaggc				gccccgcggg		670									
cgggcccctc	cccggcccctc				cggcctgccc				ggcacccccg				gacccccttg				ccccgcgggc		730									
tccccggaag	gcagcgccgc				ctgggagtgg				ggaggctgcg				gcgacgacgt				ggacttcggg		790									
gacgagaagt	cgaggctctt				tatgsacgcg				cggcacaagc				ggggacgcgg				agacatccgc		850									
gcgttggtgc	aatgcacaa				caacgaggcg				ggcaggctgg				ccgtgcggag				ccacgacgcg		910									
accgagtgc	aatgccagg				gctgtcggga				tcactgcgcg				tgcgcacttg				ctggcagaag		970									
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gtcatgggca	ccaacgacgg				caaggccctg				ctgcccgcgc				tccgcacgct				caagccgcgcg		1090									
ggccgagcgg	acctcctcta				cgccgcgcgat				tcgcccgact				tctgcgcccc				caaccgacgc		1150									
accggtccc	ccggcacgcg				cggctcgcgcc				tgcaatagca				gcgccccgga				cctcagcggc		1210									
tgcgacctgc	tgtgctgcgg				ccgcgggcac				cgccaggaga				gcgtgcagct				cgaagagaac		1270									
tgctgtgccc	gcttccactg				gtgctgcgta				gtacagtgcc				accgctgccc				tgtgcgcaag		1330									
gagctgagcc	tctgcctgtg				accgcgcgcc				cgcccgctag				actgacttcg				cgcagcgggtg		1390									
gctcgcacct	tggggacctc				agggcacccg				cacggggcgc				ctctgcgccg				tcgagcccag		1450									
cctctccctg	ccaaagccca				actcccaggg				ctctggaaat				ggtgaggcga				ggggcttgag		1510									
aggaacgccc	accacgaag				gcccagggcg				ccagacggcc				ccgaaaaggc				gctcggggag		1570									
cgtttaaagg	aactgtaca				ggccctccct				ccccttggcc				tctaggagga				aacagttttt		1630									
tagactggaa	aaaagccagt				ctaaaggcct				ctggatactg				ggctccccag				aactgctggc		1690									
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aaaa																1750												

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<210> 84
<211> 131
<212> PRT
<213> Homo sapiens
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<400> 84															
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				-20					-15						-10
Leu	Cys	Pro	Ala	His	Val	Gly	Gly	Leu	Trp	Trp	Ala	Val	Gly	Ser	Pro
			-5					1				5			
Leu	Val	Met	Asp	Pro	Thr	Ser	Ile	Cys	Arg	Lys	Ala	Arg	Arg	Leu	Ala
	10					15				20					
Gly	Arg	Gln	Ala	Glu	Leu	Cys	Gln	Ala	Glu	Pro	Glu	Val	Val	Ala	Glu
25				30					35						40
Leu	Ala	Arg	Gly	Ala	Arg	Leu	Gly	Val	Arg	Glu	Cys	Gln	Phe	Gln	Phe
			45						50					55	
Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg
			60					65					70		
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	His	Pro	Ala	Arg	Thr	Leu

75 80 85  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro  
 90 95 100  
 Gly Pro Ser  
 105

<210> 85  
 <211> 1754  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..117

<220>  
 <221> CDS  
 <222> 118..510

<220>  
 <221> 3'UTR  
 <222> 511..1754

<220>  
 <221> polyA\_signal  
 <222> 1718..1723

<220>  
 <221> polyA\_site  
 <222> 1739..1754

<400> 85  
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 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165  
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu  
 -20 -15 -10  
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213  
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
 -5 1 5  
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
 10 15 20 25  
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 30 35 40  
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
 45 50 55  
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
 75 80 85  
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Phe Gln Val Pro  
 90 95 100 105  
 ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550  
 Gly Pro Ser  
 acagacattc gggagacggc cttcgtgttc gccatcactg cggcgggcgc cagccacggc 610  
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670  
 cgggcccctc cccggccctc cggcctgccc ggcacccccg gacccccctg ccccgcgggc 730

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tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790
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gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910
accgagtgca aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
ctgcctccat ttcgcgaggt gggcgcgcg cgctgtggag gcttycacgg cgcctcacgc 1030
gtcatgggca ccaacgacgg caaggccctg ctgcccgcgg tccgcacgct caagccgcgg 1090
ggccgagcgg acctcctcta cgccgccgat tgcgccgact tctgcgcccc caaccgacgc 1150
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tgctgtgccc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgcctgtg acccgccgcc cgcccgctag actgacttcg cgcagcgggtg 1390
gctcgcacct gtgggacctc agggcacccg caccggggcg ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gccacgggcg ccagacggcc ccgaaaaggc gctcggggag 1570
cgtttaaagg aactgtaca ggccctccct ccccttggcc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatattt aaaccaccaa aaaaaaaaaa 1750
aaaa 1754

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<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
          -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
          10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
          75          80          85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
          90          95          100
Gly Pro Ser
105

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<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..151

<220>
<221> CDS
<222> 152..655

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<220>
<221> 3'UTR

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<222> 656..1431

<220>

<221> polyA\_signal

<222> 1399..1404

<220>

<221> polyA\_site

<222> 1416..1431

<400> 87

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gccccaaacca agggccccag agagggtcccc caggccccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                               Met Leu Phe Arg Leu Ser Glu
                               1           5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
          10           15           20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
          25           30           35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
          40           45           50           55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
          60           65           70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
          75           80           85
gaa gag gag gat gat gaa gaa gag gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
          90           95           100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
          105           110           115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Glu Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
          120           125           130           135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
          140           145           150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
          155           160           165
aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr
tccccagaaa cccactctat cctcaccctg ttttgtgtctc ttccccctgc ctgctagggc 765
tgcggttctt gacttctaga agactaaggc tgggtctgtgt ttgcttgttt gccaccttt 825
ggctgatacc cagagaacct gggcacttgc tgctgatgc ccacccctgc cagtcattcc 885
tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc 945
gggaacaggg atttgccctt cacaattcta ctccccagat cctctccccct ggacacagga 1005
gacccacagg gcaggaccct aagatctggg gaaaggagggt cctgagaacc ttgaggtacc 1065
cttagatcct tttctaccca ctttctctatg gaggattcca agtcaccact tctctaccg 1125
gcttctacca ggggtccagga ctaaggcggt tttctocata gcctcaacat tttgggaatc 1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tggttgcgtt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccagggt ttccttgtcc cccagctgct ctgccccctt ccccttcttc 1365
cctgactcca ggccctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa 1431
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<210> 88

<211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
 Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser  
 1 5 10 15  
 Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg  
 20 25 30  
 Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg  
 35 40 45  
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln  
 50 55 60  
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr  
 65 70 75 80  
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu  
 85 90 95  
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser  
 100 105 110  
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu  
 115 120 125  
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp  
 130 135 140  
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg  
 145 150 155 160  
 Pro Ser Pro Ser Glu Pro Gly Thr  
 165

<210> 89  
 <211> 1431  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..151

<220>  
 <221> CDS  
 <222> 152..655

<220>  
 <221> 3'UTR  
 <222> 656..1431

<220>  
 <221> polyA\_signal  
 <222> 1399..1404

<220>  
 <221> polyA\_site  
 <222> 1416..1431

<400> 89  
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 gcccaaacca agggccccag agaggtcccc caggcccctt tgggtccctg agcctcagct 120  
 ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172  
 Met Leu Phe Arg Leu Ser Glu  
 1 5  
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220  
 His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly  
 10 15 20  
 gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268

Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr  
 25 30 35  
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316  
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln  
 40 45 50 55  
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364  
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu  
 60 65 70  
 ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412  
 Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu  
 75 80 85  
 gaa gag gag gat gat gaa gaa gag gaa gaa gag gag gac agc cag gct 460  
 Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala  
 90 95 100  
 gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508  
 Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys  
 105 110 115  
 ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556  
 Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu  
 120 125 130 135  
 tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604  
 Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu  
 140 145 150  
 agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652  
 Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly  
 155 160 165  
 aca taggcaccca gcctgcatct cccaggagga agtggagggg acatcgctgt 705  
 Thr  
 tccccagaaa cccactctat cctcaccctg ttttgtgtctc ttcccctcgc ctgctagggc 765  
 tgcggtcttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccaccttt 825  
 ggcgtatacc cagagaacct gggcacttgc tgctgatgc ccaccctgc cagtcattcc 885  
 tccattcacc cagcgggagg tgggatgtga gacagccac attggaaaat ccagaaaacc 945  
 gggaacaggg atttgccctt cacaattcta ctcccagat cctctccctt ggacacagga 1005  
 gaccacaggg gcaggaccct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065  
 cttagatcct tttctacca ctttctctatg gaggattcca agtcaccact tctctcaccg 1125  
 gcttctacca ggggtccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185  
 ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245  
 tggtgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305  
 acagcggggg ggcgcaggtt ttccttgctc ccagctgct ctgccccttt ccccttcttc 1365  
 cctgactcca ggcctgaacc cctcccgctgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425  
 aaaaaa 1431

<210> 90  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
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 1 5 10 15  
 Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg  
 20 25 30  
 Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg  
 35 40 45  
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln  
 50 55 60  
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr  
 65 70 75 80  
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu  
 85 90 95  
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser  
 100 105 110  
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu

115 120 125  
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp  
 130 135 140  
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg  
 145 150 155 160  
 Pro Ser Pro Ser Glu Pro Gly Thr  
 165

<210> 91  
 <211> 1417  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..47

<220>  
 <221> CDS  
 <222> 48..1301

<220>  
 <221> 3'UTR  
 <222> 1302..1417

<220>  
 <221> polyA\_signal  
 <222> 1360..1365

<220>  
 <221> polyA\_site  
 <222> 1402..1417

<400> 91  
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 Met Pro Ser  
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104  
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
 -20 -15 -10 -5  
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152  
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr  
 1 5 10  
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200  
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr  
 15 20 25  
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248  
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His  
 30 35 40  
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296  
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr  
 45 50 55 60  
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344  
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu  
 65 70 75  
 atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag 392  
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln  
 80 85 90  
 atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac 440  
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp  
 95 100 105  
 agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc 488  
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly  
 110 115 120

[illegible]

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<210> 92
<211> 418
<212> PRT
<213> Homo sapiens
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[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

<220>  
 <221> CDS  
 <222> 278..733

<220>  
 <221> 3'UTR  
 <222> 734..1115

<220>  
 <221> polyA\_signal  
 <222> 1072..1077

<220>  
 <221> polyA\_site  
 <222> 1101..1115

<400> 93  
 ctctttgctc taacagacag cagcgacttt aggctggata atagtcaaat tcttacctcg 60  
 ctcttttact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120  
 tcttgatctg cttctaaaaa aagaagtaga gaagataaat cctgtcttca atacctggaa 180  
 ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240  
 gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295  
 Met His Phe Gly Leu Leu  
 -15  
 tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343  
 Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu  
 -10 -5 1  
 gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391  
 Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu  
 5 10 15 20  
 aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439  
 Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys  
 25 30 35  
 aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487  
 Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys  
 40 45 50  
 gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535  
 Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu  
 55 60 65  
 agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583  
 Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg  
 70 75 80  
 att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631  
 Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu  
 85 90 95 100  
 gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679  
 Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr  
 105 110 115  
 aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727  
 Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp  
 120 125 130  
 gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggt 783  
 Ala Ile  
 ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843  
 actccgcaat caaccaagggt tcccagcctt tttgttacaa aagaaggaac aaatgatggt 903  
 tggaagaatg cggctcatat ttaccaagtc tttctgaacg ccttctgcat tcatgcatcc 963  
 atgttctttc taggattgga tagcatttca tgccatgtt aatattttgtg cttttggcat 1023  
 ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083  
 atattttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94  
 <211> 152

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..19

<400> 94  
 Met His Phe Gly Leu Leu Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro  
 -15 -10 -5  
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp  
 1 5 10  
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys  
 15 20 25  
 Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn  
 30 35 40 45  
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly  
 50 55 60  
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr  
 65 70 75  
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys  
 80 85 90  
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr  
 95 100 105  
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser  
 110 115 120 125  
 Ser Met Val Asp Ala Trp Ala Ile  
 130

<210> 95  
 <211> 1307  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..252

<220>  
 <221> CDS  
 <222> 253..744

<220>  
 <221> 3'UTR  
 <222> 745..1307

<220>  
 <221> polyA\_signal  
 <222> 1269..1274

<220>  
 <221> polyA\_site  
 <222> 1292..1307

<400> 95  
 ctctttgctc taacagacag cagcgacttt aggctggata atagtcaa at tcttacctcg 60  
 ctctttcact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120  
 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180  
 ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240  
 gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291  
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala  
 -25 -20 -15  
 tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339



[illegible]

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<220>
<221> SIGNAL
<222> 1..28
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89

Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu  
85 90 95 100  
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn  
105 110 115  
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly  
120 125 130  
Asn Gln Gln Phe  
135

<210> 97  
<211> 1855  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> 1..117

<220>  
<221> CDS  
<222> 118..504

<220>  
<221> 3'UTR  
<222> 505..1855

<220>  
<221> polyA\_signal  
<222> 1819..1824

<220>  
<221> polyA\_site  
<222> 1840..1855

<400> 97  
tccccgggccg ccgccgttgc gctcgccgcg ctcgcactga agccccgggcc ctcgcgcgcc 60  
gcggttcgcc ccgcagcctc gccccctgcc caccgcggcg gccgtagggc ggtcacg 117  
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165  
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu  
-20 -15 -10  
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213  
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
-5 1 5  
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261  
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
10 15 20 25  
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309  
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
30 35 40  
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357  
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
45 50 55  
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405  
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
60 65 70  
atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453  
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu  
75 80 85  
tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501  
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val  
90 95 100 105  
gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554  
Ala

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cctcccaggc ccctgggggca gccctcccg cgcaggtttc aggtcccagg ccccagctga 614
ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
cgtgttcgcc atcaactgcg ccggcgccag ccacgcgctc acgcaggcct gttctatggg 734
cgagctgctg cagtgcgggt gccaggcgcc ccgcggggcg gcccctcccc ggccctccgg 794
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cgcgcggctg ctggagcgct tccacggcg ctcacgcgtc atgggcacca acgacggcaa 1154
ggccctgctg ccgcgcgtcc gcacgtcaa gccgccggg cgagcggacc tcctctacgc 1214
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cccagggtc tggaaatggg gagcgaggg gcttgagagg aacgccacc cacgaaggcc 1634
cagggcgcca gacggccccg aaaaggcgct cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc cttggcctct aggaggaaac agtttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tccccagaac tgctggccac aggatgggtg gtgaggttag 1814
tatcaataaa gatatttaaa ccacaaaaa aaaaaaaaaa a 1855

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<210> 98
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25 30 35 40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100
Ala
105

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<210> 99
<211> 667
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..94

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<220>
<221> CDS

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<222> 95..613

<220>

<221> 3'UTR

<222> 614..667

<220>

<221> polyA\_signal

<222> 636..641

<220>

<221> polyA\_site

<222> 652..667

<400> 99

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ctctgcaaat ccaggacaca cattgtgtc cgcgtccac taaaggcttg agtgggcact 60
gttccatctc aacagcccct gttttggaaa ggac atg att gtc aag ggg gtg gcc 115
                               Met Ile Val Lys Gly Val Ala
                               1       5
tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser
          10          15          20
tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val
          25          30          35
gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile
          40          45          50          55
ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
          60          65          70
acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
          75          80          85
aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr
          90          95          100
gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
          105          110          115
tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
          120          125          130          135
gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
          140          145          150
gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys
          155          160          165
caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643
Gln Thr Thr Val Lys Asn
          170
tctttcgcaa aaaaaaaaaa aaaa 667
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<211> 173

<212> PRT

<213> Homo sapiens

<400> 100

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Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
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ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
      75      80      85
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct 462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
      90      95      100
cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac 510
Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp
     105     110     115
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc 558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile
    120     125     130     135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag 606
Lys Lys Ser Ser Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln
      140      145      150
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg 659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu
      155      160
cctctaagcc caagccaagc catcgcatcc cctgtgactt gcacatatac gcccagatgg 719
cctgaagtaa ctgaagaatc acaaaagaag tgaaaaggcc ctgcctcgcc ttaactgatg 779
acgttccacc attgtgattt gttcctgccc caccttaact gactgattaa ccctgtgaat 839
ttccttcttc tggctcagaa gtcctccccc tgagcacctt gtgacccctt gccctgccc 899
accagagaac aacccccctt gactgtaatt ttccattacc ttcccaaata ctataaaacg 959
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 <212> PRT  
 <213> Homo sapiens

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20     25     30
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
35     40     45
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
50     55     60
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
65     70     75     80
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
85     90     95
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
100    105    110
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
115    120    125
Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys
130    135    140
Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala
145    150    155    160
Leu Leu

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<210> 103  
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 <212> DNA  
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 ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120  
 cagatgtgta cggatgaaaa tacagtggag atg agt cag aaa ccg gcc aag gag 173  
 Met Ser Gln Lys Pro Ala Lys Glu  
 1 5  
 ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221  
 Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile  
 10 15 20  
 cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269  
 His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val  
 25 30 35 40  
 gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317  
 Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys  
 45 50 55  
 gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365  
 Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg  
 60 65 70  
 aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412  
 Lys Ile Arg Pro Thr Pro Lys Lys Lys  
 75 80  
 ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccctggatga 472  
 agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532  
 gctcatgggc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592  
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 gcgtgggtggc gggcgctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832  
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 <211> 81  
 <212> PRT  
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 Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys  
 35 40 45  
 Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala  
 50 55 60  
 Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys  
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<210> 105  
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<212> DNA  
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Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys  
-10 -5 1 5  
ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca 151  
Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr  
10 15 20  
ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199  
Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr  
25 30 35  
gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247  
Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu  
40 45 50  
tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct 295  
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala  
55 60 65  
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc 343  
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro  
70 75 80 85  
aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct 391  
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala  
90 95 100  
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct 439  
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro  
105 110 115  
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca 487  
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala  
120 125 130  
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg 535  
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg  
135 140 145  
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat 583  
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn  
150 155 160 165  
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa 631  
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu  
170 175 180



tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt 679  
 Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe  
 185 190 195  
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 Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr  
 200 205 210  
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 Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu  
 215 220 225  
 tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct 823  
 Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser  
 230 235 240 245  
 tgt aaa gta cct gtg aaa aaa gcc act gtg gtg tac caa gga gag aga 871  
 Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg  
 250 255 260  
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 Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys  
 265 270 275  
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 Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu  
 280 285 290  
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 Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys  
 295 300 305  
 gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag 1063  
 Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys  
 310 315 320 325  
 cca tgc taagggtgggtt ttcagattcc acataaaaatg tcacacttgt ttcttgttca 1119  
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 Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr  
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 Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe  
 30 35 40 45  
 Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr  
 50 55 60  
 Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg  
 65 70 75  
 Tyr Thr Thr Phe Glu Tyr Pro Asn Thr Ile Ser Phe Ser Cys Asn Thr  
 80 85 90  
 Gly Phe Tyr Leu Asn Gly Ala Asp Ser Ala Lys Cys Thr Glu Glu Gly  
 95 100 105  
 Lys Trp Ser Pro Glu Leu Pro Val Cys Ala Pro Ile Ile Cys Pro Pro  
 110 115 120 125  
 Pro Ser Ile Pro Thr Phe Ala Thr Leu Arg Val Tyr Lys Pro Ser Ala  
 130 135 140  
 Gly Asn Asn Ser Leu Tyr Arg Asp Thr Ala Val Phe Glu Cys Leu Pro





Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln  
                     400                    405                    410  
 gca cct gac atc gac gtg cag ctg agc tcg gag ctg aca gac tcg ctc 1299  
 Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu  
                     415                    420                    425  
 agg acc ctg aag ccc gag ggc aac atc ctt cga gac cgg ttc aag agc 1347  
 Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser  
                     430                    435                    440  
 ttc cag agg agg aat atg atc gag cct cga gag aga gcc aag ttc aaa 1395  
 Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys  
                     445                    450                    455                    460  
 cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc 1443  
 Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile  
                     465                    470                    475  
 cag ttg tagctgccat cagatgccgg agactcgccc ttcaataaaaa aatctcttct 1499  
 Gln Leu  
 agctcaaaaa aaaaaaaaaa a 1520

<210> 108  
 <211> 478  
 <212> PRT  
 <213> Homo sapiens

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 Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp  
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 Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu  
                     50                    55                    60  
 Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu  
   65                    70                    75                    80  
 Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys  
                     85                    90                    95  
 Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu  
                     100                    105                    110  
 Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val  
                     115                    120                    125  
 Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys  
                     130                    135                    140  
 Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu  
   145                    150                    155                    160  
 Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser  
                     165                    170                    175  
 Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe  
                     180                    185                    190  
 Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly  
                     195                    200                    205  
 Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg  
                     210                    215                    220  
 Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val  
   225                    230                    235                    240  
 Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr  
                     245                    250                    255  
 Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala  
                     260                    265                    270  
 Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr Glu Gln Ala Ala  
                     275                    280                    285  
 Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu  
                     290                    295                    300  
 Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly



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Tyr	Gln	Ser	Asp	Glu	Thr	Leu	Pro	Ile	Asn	Pro	Leu	Ser	Met	Leu	Leu	
		60					65					70				
aac	ggg	att	gtg	gac	cct	gct	gtc	atg	gga	ggc	ttc	gcc	aag	tat	gag	403
Asn	Gly	Ile	Val	Asp	Pro	Ala	Val	Met	Gly	Gly	Phe	Ala	Lys	Tyr	Glu	
		75					80					85				
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Lys	Ala	Phe	Phe	Thr	Glu	Glu	Tyr	Val	Arg	Asp	His	Pro	Glu	Asp	Gln	
		90				95				100					105	
gac	aag	ctg	acc	cac	ctc	aag	gac	ctg	att	gca	tgg	cag	atc	ccc	ttc	499
Asp	Lys	Leu	Thr	His	Leu	Lys	Asp	Leu	Ile	Ala	Trp	Gln	Ile	Pro	Phe	
			110						115						120	
ttg	gga	gct	ggg	att	aag	atc	cat	gag	aaa	agg	gtg	tca	gat	aac	ttg	547
Leu	Gly	Ala	Gly	Ile	Lys	Ile	His	Glu	Lys	Arg	Val	Ser	Asp	Asn	Leu	
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cga	ccc	ttc	cat	gac	cgg	atg	gag	gaa	tgt	ttc	aag	aac	ctg	aaa	atg	595
Arg	Pro	Phe	His	Asp	Arg	Met	Glu	Glu	Cys	Phe	Lys	Asn	Leu	Lys	Met	
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Lys	Val	Glu	Lys	Glu	Tyr	Gly	Val	Arg	Glu	Met	Pro	Asp	Phe	Asp	Asp	
		155					160					165				
agg	aga	gtg	ggc	cgt	ccc	agg	tct	atg	ctg	cgc	tca	tac	aga	cag	atg	691
Arg	Arg	Val	Gly	Arg	Pro	Arg	Ser	Met	Leu	Arg	Ser	Tyr	Arg	Gln	Met	
		170			175					180					185	
tcc	atc	atc	tct	ctg	gct	tcc	atg	aat	tct	gac	tgc	agc	acc	ccc	agc	739
Ser	Ile	Ile	Ser	Leu	Ala	Ser	Met	Asn	Ser	Asp	Cys	Ser	Thr	Pro	Ser	
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aag	cct	acc	tca	gag	agc	ttt	gac	ctg	gaa	tta	gca	tca	ccc	aag	acg	787
Lys	Pro	Thr	Ser	Glu	Ser	Phe	Asp	Leu	Glu	Leu	Ala	Ser	Pro	Lys	Thr	
		205						210					215			
ccg	aga	gtg	gag	cag	gag	gaa	ccg	atc	tcc	ccg	ggg	agc	acc	ctg	cct	835
Pro	Arg	Val	Glu	Gln	Glu	Glu	Pro	Ile	Ser	Pro	Gly	Ser	Thr	Leu	Pro	
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Glu	Val	Lys	Leu	Arg	Arg	Ser	Lys	Lys	Arg	Thr	Lys	Arg	Ser	Ser	Val	
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Val	Phe	Ala	Asp	Glu	Lys	Ala	Ala	Ala	Glu	Ser	Asp	Leu	Lys	Arg	Leu	
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Ser	Arg	Lys	His	Glu	Phe	Met	Ser	Asp	Thr	Asn	Leu	Ser	Glu	His	Ala	
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gcc	atc	ccc	ctc	aag	gcg	tct	gtc	ctc	tct	caa	atg	agc	ttt	gcc	agc	1027
Ala	Ile	Pro	Leu	Lys	Ala	Ser	Val	Leu	Ser	Gln	Met	Ser	Phe	Ala	Ser	
			285					290							295	
cag	tcc	atg	cct	acc	atc	cca	gcc	ctg	gcg	ctc	tca	gtg	gca	ggc	atc	1075
Gln	Ser	Met	Pro	Thr	Ile	Pro	Ala	Leu	Ala	Leu	Ser	Val	Ala	Gly	Ile	
		300					305					310				
cct	ggg	ttg	gat	gag	gcc	aac	aca	tct	ccc	cgc	ctc	agc	cag	acc	ttc	1123
Pro	Gly	Leu	Asp	Glu	Ala	Asn	Thr	Ser	Pro	Arg	Leu	Ser	Gln	Thr	Phe	
		315					320					325				
ctc	caa	ctc	tca	gat	ggt	gac	aag	aag	aca	ctc	aca	cgg	aag	aag	gtc	1171
Leu	Gln	Leu	Ser	Asp	Gly	Asp	Lys	Lys	Thr	Leu	Thr	Arg	Lys	Lys	Val	
		330			335					340					345	
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Asn	Gln	Phe	Phe	Lys	Thr	Met	Leu	Ala	Ser	Lys	Ser	Ala	Glu	Glu	Gly	
			350						355						360	
aaa	cag	atc	cca	gac	tcg	ctg	tcc	acg	gac	ctg	tgagctgctg	ctgactaggg				1272
Lys	Gln	Ile	Pro	Asp	Ser	Leu	Ser	Thr	Asp	Leu						
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aagcctcaga	gagtgggaga	ctgtcccat	cagttgtcct	tacttagagg	agacagagag											1392

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ctcccagtgt gctctcccca acatcctagg cacagctttc ataaccagc ttcttaggtg 1572
taagaaactg tttttatctc atttattaag tctcagaact taacagaaaa ggaagccttt 1632
taaatattct ttttaatttt atttttagatt aacagttttg tactttacat ttttttatac 1692
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<210> 110
<211> 386
<212> PRT
<213> Homo sapiens

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<220>
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<222> 1..15

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Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
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Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
35 40 45
Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
50 55 60 65
Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
70 75 80
Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
85 90 95
Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
100 105 110
Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
115 120 125
Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
130 135 140 145
Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
150 155 160
Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
165 170 175
Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
180 185 190
Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
195 200 205
Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
210 215 220 225
Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
230 235 240
Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
245 250 255
Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
260 265 270
Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
275 280 285
Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
290 295 300 305
Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
310 315 320
Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
325 330 335
Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala

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Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val	
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atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt	642
Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu	
165 170 175 180	
ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act	690
Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr	
185 190 195	
gtg gag gtc aca aag acg ttt ttg cct ctt ctt aga aaa tcc aaa ggg	738
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly	
200 205 210	
agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg	786
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg	
215 220 225	
ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca	834
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser	
230 235 240	
gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc	882
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile	
245 250 255 260	
caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg	930
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp	
265 270 275	
gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag	978
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln	
280 285 290	
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta	1026
Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu	
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Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp	
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atc cag cat gct atc ttg gcg aag agc cct ttt gcc tat tac acg cca	1122
Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro	
325 330 335 340	
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Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile	
345 350 355	
ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc	1218
Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro	
360 365 370	
atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc	1263
Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Lys Ala Pro	
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<210> 112

<211> 387

<212> PRT

<213> Homo sapiens

<400> 112

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35 40 45	
Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser	
50 55 60	

Cys	Phe	Leu	Met	Tyr	Thr	Tyr	Leu	Ser	Gly	Gln	Glu	Leu	Leu	Pro	Val
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Asp	Gln	Lys	Ala	Val	Leu	Val	Thr	Gly	Gly	Asp	Cys	Gly	Leu	Gly	His
			85						90					95	
Ala	Leu	Cys	Lys	Tyr	Leu	Asp	Glu	Leu	Gly	Phe	Thr	Val	Phe	Ala	Gly
			100					105					110		
Val	Leu	Asn	Glu	Asn	Gly	Pro	Gly	Ala	Glu	Glu	Leu	Arg	Arg	Thr	Cys
		115					120					125			
Ser	Pro	Arg	Leu	Ser	Val	Leu	Gln	Met	Asp	Ile	Thr	Lys	Pro	Val	Gln
	130					135						140			
Ile	Lys	Asp	Ala	Tyr	Ser	Lys	Val	Ala	Ala	Met	Leu	Gln	Asp	Arg	Gly
145					150					155					160
Leu	Trp	Ala	Val	Ile	Asn	Asn	Ala	Gly	Val	Leu	Gly	Phe	Pro	Thr	Asp
			165						170					175	
Gly	Glu	Leu	Leu	Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn
			180					185					190		
Phe	Phe	Gly	Thr	Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg
	195						200					205			
Lys	Ser	Lys	Gly	Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala
	210					215					220				
Pro	Val	Glu	Arg	Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr
225					230					235					240
Met	Phe	Ser	Ser	Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys
			245						250					255	
Val	Ala	Ser	Ile	Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr
			260					265					270		
Ser	Asp	Lys	Trp	Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro
	275						280					285			
Ala	Glu	Val	Gln	Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg
	290					295					300				
Asn	Phe	Leu	Leu	Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro
305					310					315					320
Val	Leu	Arg	Asp	Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala
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Tyr	Tyr	Thr	Pro	Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His
			340					345					350		
Tyr	Leu	Pro	Ile	Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly
	355						360					365			
Gln	Asp	Lys	Pro	Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys
	370					375					380				
Lys	Ala	Pro													
385															